

GenCore version 5.1.6  
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protein - protein search, using sw model

on: December 16, 2003, 15:36:20 ; Search time 14.5792 Seconds  
(without alignments)  
266.996 Million cell updates/sec

le: US-09-920-137A-7

fect score: 486  
rence: 1 MKLCVTLSLLMLVAFCSP.....VCADPSBSWQEVYVDLELN 92

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 328717 seqs, 42310858 residues

al number of hits satisfying chosen parameters: 328717

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pap.\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pap.\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pap.\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pap.\*

5: /cgn2\_6/ptodata/1/1aa/PTCUS\_COMB.pap.\*

6: /cgn2\_6/ptodata/1/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	92	1	US-08-347-492B-11
2	486	100.0	92	1	US-08-375-346A-4
3	486	100.0	92	2	US-08-421-144A-4
4	486	100.0	92	2	US-08-798-143-11
5	486	100.0	92	2	US-08-467-123B-4
6	486	100.0	92	3	US-08-808-720-10
7	486	100.0	92	3	US-09-133-521-6
8	486	100.0	92	4	US-08-679-493A-157
9	486	100.0	92	4	US-08-679-493A-158
10	486	100.0	92	4	US-09-230-371A-24
11	486	100.0	331	3	US-08-808-720-7
12	482	99.2	92	3	US-09-230-637-41
13	482	99.2	92	4	US-08-679-493A-159
14	476	97.9	92	1	US-07-792-988-2
15	461	94.9	92	4	US-08-649-006A-9
16	461	94.9	92	4	US-09-771-023-11
17	457	94.0	92	4	US-08-679-493A-160
18	448.5	92.3	91	1	US-08-480-449-22
19	448.5	92.3	91	2	US-08-660-542-22
20	448.5	92.3	91	4	US-08-479-603-22
21	448.5	92.3	91	4	US-08-939-107-22
22	394	81.1	92	4	US-09-198-106-3
23	375	77.2	69	3	US-07-982-759F-35
24	375	77.2	74	2	US-08-450-905B-35
25	371	76.3	68	2	US-08-615-232A-10
26	371	76.3	68	3	US-08-470-323-10
27	359	73.9	69	2	US-08-716-188-6

Sequence 15, Appl  
Sequence 15, Appl  
Sequence 4, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 2, Appl  
Sequence 5, Appl  
Sequence 6, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 23, Appl  
Sequence 6, Appl  
Sequence 1, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 10, Appl  
Sequence 3, Appl  
Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-347-492B-11  
; Sequence 11, Application US/08347492B  
; Patent No. 5603008  
; GENERAL INFORMATION:  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
; TITLE OF INVENTION: PRODUCTION AND USES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,492B  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/303,241  
; FILING DATE: 07-SEP-1994  
; APPLICATION NUMBER: 08/320,011  
; FILING DATE: 05-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 92 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: GI 127080  
US-08-347-492B-11

Tue Dec 16 15:54:07 2003

Query Match 100.0%; Score 486; DB 1; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKLCVTLSLLMLVAAFCSPPALSAPMGSDPTACCFSTARKLPNRFVVDYETSSLSQ 60  
1 MKLCVTLSLLMLVAAFCSPPALSAPMGSDPTACCFSTARKLPNRFVVDYETSSLSQ 60

61 PAVVFQTKRSKQVCADPSESWMQVEYVVDLELN 92  
61 PAVVFQTKRSKQVCADPSESWMQVEYVVDLELN 92

SULT 2  
-08-375-346A-4  
Sequence 4, Application US/08375346A  
Patent No. 5605817  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig G.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
TITLE OF INVENTION: ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,346A  
FILING DATE: 19-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0026 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 855-0572  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
-08-375-346A-4

Query Match 100.0%; Score 486; DB 1; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKLCVTLSLLMLVAAFCSPPALSAPMGSDPTACCFSTARKLPNRFVVDYETSSLSQ 60  
1 MKLCVTLSLLMLVAAFCSPPALSAPMGSDPTACCFSTARKLPNRFVVDYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWMQVEYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWMQVEYVVDLELN 92

RESULT 3  
US-08-421-144A-4  
Sequence 4, Application US/08421144A  
Patent No. 5874211  
GENERAL INFORMATION:  
APPLICANT: BANDMAN, OLGA  
APPLICANT: COLEMAN, ROGER  
APPLICANT: STUART, SUSAN G.  
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN BOSINOPHILS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,144A  
FILING DATE: 13-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF-0031 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-421-144A-4

Query Match 100.0%; Score 486; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAFCSPPALSAPMGSDPTACCFSTARKLPNRFVVDYETSSLSQ 60  
Db 1 MKLCVTLSLLMLVAAFCSPPALSAPMGSDPTACCFSTARKLPNRFVVDYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWMQVEYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWMQVEYVVDLELN 92

RESULT 4  
US-08-798-143-11  
Sequence 11, Application US/08798143  
Patent No. 5936068  
GENERAL INFORMATION:  
APPLICANT: Wilde, Craig G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
TITLE OF INVENTION: PRODUCTION AND USES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,143  
 FILING DATE: 10-FEB-1997

## CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/347,452  
 FILING DATE: 29-NOV-1994  
 APPLICATION NUMBER: 08/303,241  
 FILING DATE: 07-SEP-1994  
 APPLICATION NUMBER: 08/320,011  
 FILING DATE: 05-OCT-1994

## ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J  
 REGISTRATION NUMBER: 33,954  
 REFERENCE/DOCKET NUMBER: PF-0024  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-852-0195

## INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 92 amino acids  
 TYPE: amino acid

## STRANDEDNESS: single

## TOPOLOGY: linear

## MOLECULE TYPE: peptide

## IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: GI 127080

-08-798-143-11

## Query Match

Best Local Similarity 100.0%; Score 486; DB 2; Length 92;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKLCVTLSLLMLVAAPSPALSGSDPTACCFSTARKLPNFVVDYVYETSSLCQ 60  
 1 MKLCVTLSLLMLVAAPSPALSGSDPTACCFSTARKLPNFVVDYVYETSSLCQ 60

61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

## RESULT 5

-08-467-123B-4  
 Sequence 4, Application US/08467123B  
 Patent No. 5945506

## GENERAL INFORMATION:

APPLICANT: Coleman, Roger  
 APPLICANT: Wilde, Craig C.  
 APPLICANT: Sellhammer, Jeffrey J.  
 TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
 ITS PRODUCTION AND USES

## NUMBER OF SEQUENCES: 9

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,123B  
 FILING DATE: 06-JUN-1995

## CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/375,346  
 FILING DATE: 19-JAN-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0026-1 DIV  
 TELEPHONE: 415-555-0555  
 TELEFAX: 415-845-4166

## INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 92 amino acids  
 TYPE: amino acid

## STRANDEDNESS: single

## TOPOLOGY: linear

## MOLECULE TYPE: peptide

US-08-467-123B-4

## Query Match

Best Local Similarity 100.0%; Score 486; DB 2; Length 92;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAPSPALSGSDPTACCFSTARKLPNFVVDYVYETSSLCQ 60  
 DB 1 MKLCVTLSLLMLVAAPSPALSGSDPTACCFSTARKLPNFVVDYVYETSSLCQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

DB 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

## RESULT 6

US-08-808-720-10  
 Sequence 10, Application US/08808720  
 Patent No. 6100387

## GENERAL INFORMATION:

APPLICANT: Herrmann, Steve  
 APPLICANT: Swanberg, Stephen  
 TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
 TITLE OF INVENTION: CHEMOKINE DOMAINS  
 NUMBER OF SEQUENCES: 10

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.  
 STREET: 87 Cambridgepark  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/808,720  
 FILING DATE:

## CLASSIFICATION: 530

## ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne  
 REGISTRATION NUMBER: P-41,323  
 REFERENCE/DOCKET NUMBER: G15291  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8284  
 TELEFAX: (617) 876-5851

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
3-08-808-720-10

Query Match 100.0%; Score 486; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
/ 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
/ 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
/ 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92  
/ 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92

## RESULT 7

3-09-133-521-6  
Sequence 6, Application US/09133521  
Patent No. 6281200

## GENERAL INFORMATION:

APPLICANT: Eife, Kenneth H.  
APPLICANT: Krathwohl, Mitchell D.

APPLICANT: Brown, Robert  
APPLICANT: Brown, Dairon R.

APPLICANT: Broxmeyer, Hal E.  
TITLE OF INVENTION: FUNCTIONAL CHARACTERIZATION OF THE C-C CHEMOKINE-LIKE

TITLE OF INVENTION: MOLECULES ENCODED BY MOLLUSCUM CONTAGIOSUM VIRUS TYPES 1

TITLE OF INVENTION: AND 2  
FILE REFERENCE: INDY-034

CURRENT APPLICATION NUMBER: US/09/133,521  
CURRENT FILING DATE: 1998-08-18

EARLIER APPLICATION NUMBER: 60/055,532  
EARLIER FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 6  
LENGTH: 92

TYPE: PRT  
ORGANISM: Homo sapiens

3-09-133-521-6  
Query Match 100.0%; Score 486; DB 3; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
/ 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
/ 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
/ 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92  
/ 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92

## RESULT 8

3-08-679-493A-157  
Sequence 157, Application US/08679493A  
Patent No. 6303295

## GENERAL INFORMATION:

APPLICANT: Taylor, Ethan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS

FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A

CURRENT FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203

PRIOR FILING DATE: 1995-07-14

; PRIOR APPLICATION NUMBER: 60/003,112  
; PRIOR FILING DATE: 1995-09-01  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 157  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-679-493A-157

Query Match 100.0%; Score 486; DB 4; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
QY 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92

## RESULT 9

US-08-679-493A-158

; Sequence 158, Application US/08679493A  
; Patent No. 6303295

## GENERAL INFORMATION:

APPLICANT: Taylor, Ethan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS

FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A

PRIOR FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203

PRIOR FILING DATE: 1995-07-14  
PRIOR APPLICATION NUMBER: 60/003,112

NUMBER OF SEQ ID NOS: 216  
SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 158  
LENGTH: 92

TYPE: PRT  
ORGANISM: Homo sapiens

US-08-679-493A-158  
Query Match 100.0%; Score 486; DB 4; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
QY 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92

## RESULT 10

US-09-230-371A-24

; Sequence 24, Application US/09230371A  
; Patent No. 6348586

## GENERAL INFORMATION:

APPLICANT: Chang, Yuan  
APPLICANT: Bohenzky, Roy A

APPLICANT: Russo, James J  
APPLICANT: Edelman, Isidore S

APPLICANT: Moore, Patrick S  
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND

FILE REFERENCE: 45185-G-PCT-US  
CURRENT APPLICATION NUMBER: US/09/230,371A

CURRENT FILING DATE: 1999-11-17

PRIOR APPLICATION NUMBER: PCT/US97/13346  
 PRIOR FILING DATE: 1997-07-22  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 24  
 LENGTH: 92  
 TYPE: PRT  
 ORGANISM: Human  
 3-09-230-371A-24

Query Match 100.0%; Score 486; DB 4; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPTACCFSTARKLPNFWVDYVYETSSLSQ 60  
 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPTACCFSTARKLPNFWVDYVYETSSLSQ 60  
 61 PAVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
 61 PAVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 11  
 3-08-808-720-7  
 Sequence 7, Application US/08808720  
 Patent No. 6100387  
 GENERAL INFORMATION:  
 APPLICANT: Herrmann, Steve  
 APPLICANT: Swenberg, Stephen  
 TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
 TITLE OF INVENTION: CHEMOKINE DOMAINS  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genetics Institute, Inc.  
 STREET: 87 CambridgePark  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 APPLICATION NUMBER: US/08/808,720  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sprunger, Suzanne  
 REGISTRATION NUMBER: P-41,323  
 REFERENCE/DOCKET NUMBER: G15291  
 TELEPHONE: (617) 498-8284  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 331 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 3-08-808-720-7

Query Match 100.0%; Score 486; DB 3; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-50;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPTACCFSTARKLPNFWVDYVYETSSLSQ 60  
 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPTACCFSTARKLPNFWVDYVYETSSLSQ 60

QY 61 PAVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
 DB 61 PAVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 12  
 US-09-230-637-41  
 Sequence 41, Application US/09230637  
 Patent No. 6264958  
 GENERAL INFORMATION:  
 APPLICANT: Hayward, Gary  
 APPLICANT: Nicholas, John  
 APPLICANT: Hardwick, J. Marie  
 APPLICANT: Reitz, Marvin  
 TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma  
 TITLE OF INVENTION: Associated Herpesvirus  
 FILE REFERENCE: 1107.78372  
 CURRENT APPLICATION NUMBER: US/09/230,637  
 CURRENT FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: 60/022,591  
 PRIOR FILING DATE: 1996-07-25  
 PRIOR APPLICATION NUMBER: PCT US 97/12931  
 PRIOR FILING DATE: 1997-07-24  
 NUMBER OF SEQ ID NOS: 62  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 41  
 LENGTH: 92  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-230-637-41

Query Match 99.2%; Score 482; DB 3; Length 92;  
 Best Local Similarity 98.9%; Pred. No. 3.9e-50;  
 Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPTACCFSTARKLPNFWVDYVYETSSLSQ 60  
 DB 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPTACCFSTARKLPNFWVDYVYETSSLSQ 60  
 QY 61 PAVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
 DB 61 PAVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 13  
 US-08-679-493A-159  
 Sequence 159, Application US/08679493A  
 Patent No. 6303295  
 GENERAL INFORMATION:  
 APPLICANT: Taylor, Ethan W.  
 TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
 FILE REFERENCE: 55-95  
 CURRENT APPLICATION NUMBER: US/08/679,493A  
 CURRENT FILING DATE: 1996-07-12  
 PRIOR APPLICATION NUMBER: 60/001203  
 PRIOR FILING DATE: 1995-07-14  
 PRIOR APPLICATION NUMBER: 60/003,112  
 PRIOR FILING DATE: 1995-09-01  
 NUMBER OF SEQ ID NOS: 216  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 159  
 LENGTH: 92  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-08-679-493A-159

Query Match 99.2%; Score 482; DB 4; Length 92;  
 Best Local Similarity 98.9%; Pred. No. 3.9e-50;  
 Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPTACCFSTARKLPNFWVDYVYETSSLSQ 60  
 DB 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPTACCFSTARKLPNFWVDYVYETSSLSQ 60

61 PAVVFQTKRSKQVCADPSESWMQVEYVDLELN 92  
 |||||  
 61 PAVVFQTKRSKQVCADPSESWMQVEYVDLELN 92

## RESULT 14

3-07-792-988-2

Sequence 2, Application US/07792988

Patent No. 5306709

GENERAL INFORMATION:

APPLICANT: Gewirtz, Alan M.

TITLE OF INVENTION: Suppression of megakaryo-

TITLE OF INVENTION: cytopoiesis by macrophage inflammatory proteins

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: University of Pennsylvania

STREET: Suite 419

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19104-3246

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07792,988

FILING DATE: 19911115

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-159

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5306709e

INFORMATION FOR SEQ ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 92 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single stranded

TOPOLOGY: linear

3-07-792-988-2

Query Match 97.9%; Score 476; DB 1; Length 92;

Best Local Similarity 98.9%; Pred. No. 2e-49;

Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKLCVTVLSLLMLVAAFCSALSPALSGSDPPTACCFSTARKLPNFWVDYETSSLCSSQ 60

1 MKLCVTVLSLLMLVAAFCSALSPALSGSDPPTACCFSTARKLPNFWVDYETSSLCSSQ 60

61 PAVVFQTKRSKQVCADPSESWMQVEYVDLELN 92

|||||

61 PAVVFQTKRSKQVCADPSESWMQVEYVDLELN 92

|||||

## RESULT 15

3-08-649-006A-9

Sequence 9, Application US/08649006A

Patent No. 6548654

GENERAL INFORMATION:

APPLICANT: Hardiman, Gerard T.

APPLICANT: Rossi, Devora L.

APPLICANT: Bacon, Kevin B.

APPLICANT: Bazan, J. Fernando

GenCore version 5.1.6  
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protein - protein search, using sw model

on: December 16, 2003, 15:36:20 ; Search time 13.4262 seconds  
 (without alignments)  
 651.810 Million cell updates/sec

le: US-09-920-137A-8

fect score: 478

quence: 1 MKVSAARLAVILIATLALCAP.....VCANPEKKWREYINSLEMS 91

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283308 seqs, 96168682 residues

al number of hits satisfying chosen parameters: 283308

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	472	98.7	91	1 A28815	monocyte chemoattr
2	393	82.2	91	1 A46539	monocyte chemoattr
3	254.5	53.2	92	2 I46730	immune activation
4	252.5	52.8	93	2 B35673	LD78-beta protein
5	248	51.9	92	2 A30574	macrophage inflam
6	248	51.9	92	2 I52322	macrophage inflam
7	245.5	51.4	92	2 C30552	macrophage inflam
8	243	50.8	92	2 A32353	macrophage inflam
9	242.5	50.7	92	1 A31757	eotaxin precursor
10	168	35.1	97	2 JC4912	monocyte chemoattr
11	167	34.9	109	2 A54678	monocyte chemoattr
12	162	33.9	120	2 I48147	monocyte chemoattr
13	156	32.6	148	1 S07723	immediate-early se
14	155	32.4	99	2 JC5295	monocyte chemoattr
15	152	31.8	99	2 JC2136	monocyte chemoattr
16	148	31.0	50	2 C60407	monocyte chemoattr
17	147	30.8	97	2 A48093	monocyte adherence
18	146.5	30.6	148	1 A30209	monocytic cytokine
19	144.5	30.2	120	2 JE0177	PDGF-inducible JE
20	144	30.1	99	1 A39236	lymphocyte and mon
21	144	30.1	99	2 JC2336	monocyte chemoattr
22	143.5	30.0	99	2 JC2417	monocyte chemoattr
23	142	29.7	96	2 I48099	monocyte chemoattr
24	141	29.5	96	2 JC2478	eotaxin precursor
25	140	29.3	99	2 A60299	monocyte chemoattr
26	140	29.3	125	2 I46857	monocyte chemoattr
27	125.5	26.3	116	2 I49855	gene C10 protein -
28	116	24.3	114	1 E2HUL	lymphotactin precu
29	107.5	22.5	92	2 S24236	TCA3 protein - mou

*Handwritten signature*

## ALIGNMENTS

## RESULT 1

A28815  
 monocyte chemoattractant cytokine RANTES precursor - human  
 N/Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Jun-1989 #sequence\_revision 16-Aug-1996 #text\_change 29-May-1998  
 C/Accession: A28815  
 R/Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.; K  
 J. Immunol. 141, 1018-1025, 1988  
 A/Title: A human T cell-specific molecule is a member of a new gene family.  
 A/Reference number: A28815; MUID:88285659; PMID:2456327  
 A/Accession: A28815  
 A/Molecule type: mRNA  
 A/Residues: 1-91 <SCH>  
 A/Cross-references: GB:M21121  
 C/Comment: The acronym RANTES reflects the description "Regulated upon Activation, Norm  
 A/Genetics:  
 A/Gene: GDB:SCYA5; D17S136E  
 A/Map position: 17q11.2-17q12  
 C/Superfamily: macrophage inflammatory protein  
 C/Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell  
 F/1-23/Domain: signal sequence #status predicted <SIG>  
 F/24-91/Product: T-cell protein RANTES #status predicted <MAT>

Query Match 98.7%; Score 472; DB 1; Length 91;  
 Best Local Similarity 98.9%; Pred. No. 2.4e-44;  
 Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
 Db 1 MKVSAARLAVILIATLALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
 QY 61 AVVFTVRKRVQVCANPEKKWREYINSLEMS 91  
 Db 61 AVVFTVRKRVQVCANPEKKWREYINSLEMS 91

## RESULT 2

A46539  
 monocyte chemoattractant cytokine RANTES precursor - mouse  
 N/Alternate names: Murantes  
 C/Species: Mus musculus (house mouse)  
 C/Date: 18-Jun-1993 #sequence\_revision 16-Aug-1996 #text\_change 22-Jun-1999  
 C/Accession: I48875; A46539; I48654; I56970  
 R/Danoff, T.M.; Lalle, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.  
 J. Immunol. 152, 1182-1189, 1994  
 A/Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene  
 A/Reference number: I48875; MUID:94132613; PMID:7507961  
 A/Accession: I48875  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA

interleukin-8 prec  
 cytokine SDF-1-bet  
 interleukin-8 - do  
 Neutrophil attract  
 interleukin-8 prec  
 interleukin-8 prec  
 pre-B-cell growth-  
 interleukin-8 homo  
 cytokine - mouse  
 I-309 protein prec  
 lymphotactin precu  
 interleukin-8 - ra  
 monocyte chemoattr  
 transformation-ind  
 RSV-induced protei  
 hypothetical prote

30 107 22.4 101 2 542496  
 31 106.5 22.3 93 2 G01540  
 32 105 22.0 95 2 JN0841  
 33 103 21.5 101 2 I48148  
 34 103 21.5 103 2 A53096  
 35 100 20.9 99 2 A37034  
 36 99 20.7 89 2 A53497  
 37 99 20.7 89 2 I53416  
 38 99 20.7 93 2 I81182  
 39 96.5 20.2 96 2 A37236  
 40 95 19.9 114 1 ETMSL  
 41 92 19.2 101 2 I46871  
 42 86.5 18.1 72 2 A55984  
 43 69 14.4 103 2 A26736  
 44 69 14.4 103 2 I50417  
 45 66 13.8 336 2 I22187

Residues: 1-91 <DAN>  
Cross-references: EMBL:U02298; NID:G460090; PIDN:AAA18302.1; PID:G460091  
Schall, T.J.; Simpson, N.J.; Mak, J.Y.  
C. J. Immunol. 22, 1477-1481, 1992  
Title: Molecular cloning and expression of the murine RANTES cytokine: structural and reference number: A46539; MUID:192289805; PMID:1376260  
Accession: A46539  
Molecule type: mRNA  
Residues: 1-18, 'A', 20-91 <SCH>  
Cross-references: GB:S37648; NID:G250207; PIDN:AAB22330.1; PID:G250208  
Experimental source: macrophage cell line PUS-1.8  
Note: Sequence extracted from NCBI backbone (NCBI:106768, NCBIP:106770)  
Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Panzacas, W.A.  
L. Cell. Biol. 14, 2914-2925, 1994  
Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking region reference number: I48654; MUID:194217689; PMID:7513046  
Accession: I48654  
Status: translation not shown; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-91 <SHI>  
Cross-references: EMBL:X70675; NID:G475205; PIDN:CAA50011.1; PID:G475206  
Jellison, E.G.; Krensky, A.  
J. Exp. Med. 175, 220-225, 1992  
Title: Isolation and characterization of cDNA from renal tubular epithelium encoding m reference number: I56970; MUID:92277990; PMID:1375672  
Accession: I56970  
Status: translated from GB/EMBL/DBJ  
Molecule type: mRNA  
Residues: 1-40, 'E', 42-91 <NEI>  
Cross-references: GB:M77747; NID:G200649; PIDN:AAA40029.1; PID:G200650  
Comment: This chemoattractant for monocytes but not neutrophils is an immediate-early phenetic:  
Introns: 26/1; 63/2  
Superfamily: macrophage inflammatory protein  
Keywords: chemotaxis; cytokine; immediate-early protein; inflammation  
-23/Domain: signal sequence #status predicted <SIG>  
4-91/Product: monocyte chemoattractant cytokine RANTES #status predicted <MAT>  
Query Match 82.2%; Score 393; DB 1; Length 91;  
Best Local Similarity 79.1%; Pred. No. 9.7e-36;  
Matches 72; Conservative 7; Mismatches 12; Indels 0; Gaps 0;  
1 MKVSAARLAVILIALCAPASASPYSDTTPCCPAYIARPLPRAHIKEYFTYSGKCSNP 60  
1 MKISAATLITLAAALCTPAPASVGSDDTTPCCPAYLSLALPRAHVKEYFTYSGKCSNL 60  
61 AVVFTVRNQRQVCANPEKKVREYINLSLEMS 91  
61 AVVFTVRNQRQVCANPEKKVQVEYINLSLEMS 91  
Mune activation gene 2 - rabbit  
Species: Oryctolagus cuniculus (domestic rabbit)  
Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 16-Jul-1999  
Accession: I46730  
Ori, S.; Goto, K.; Goto, F.; Murakami, K.; Ohkawara, S.; Yoshinaga, M.  
Immunol. 6, 149-156, 1994  
Title: Dynamic changes in mRNA expression of neutrophils during the course of acute in ference number: I46730; MUID:94198229; PMID:8148323  
Accession: I46730  
Status: preliminary; translated from GB/EMBL/DBJ  
Molecule type: mRNA  
Residues: 1-92 <MOR>  
Cross-references: GB:D17402; NID:G599577; PIDN:BA04226.1; PID:G599578  
Superfamily: macrophage inflammatory protein  
Query Match 53.2%; Score 254.5; DB 2; Length 92;  
Best Local Similarity 51.1%; Pred. No. 1.2e-20;  
Matches 47; Conservative 16; Mismatches 28; Indels 1; Gaps 1;  
1 MKVSAARLAVILIALCAPASASPYSSD-TTPCCPAYIARPLPRAHIKEYFTYSGKCSN 59

Db 1 MKLGVTVLVALLVAALCPALAPMGSDPTACCSYTLRKLPRIHVIDYFETTSLSQ 60  
Qy 60 PAVVFTVRNQRQVCANPEKKVREYINLSLEMS 91  
Db 61 PAVVFTQTKGRQVCANPESVQVEYVDLEIN 92  
RESULT 4  
B35673  
LD78-beta protein precursor - human  
N/Alternate names: macrophage inflammatory protein homolog GOS19-2; small inducible cyt C/Species: Homo sapiens (man)  
C/Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 20-Jun-2000  
C/Accession: B35673; B30412; S10157; B30908  
R/Nakao, M.; Nomiya, H.; Shimada, K.  
Mol. Cell. Biol. 10, 3646-3658, 1990  
A/Title: Structures of human genes coding for cytokine LD78 and their expression.  
A/Reference number: A35673; MUID:90287155; PMID:1694014  
A/Accession: B35673  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-93 <NAK>  
A/Cross-references: GB:D90145; NID:G219907; PIDN:BA04173.1; PID:G219908  
R/Blum, S.; Forsdyke, R.E.; Forsdyke, D.R.  
DNA Cell Biol. 9, 589-602, 1990  
A/Title: Three human homologs of a murine gene encoding an inhibitor of stem cell proli A/Reference number: A30412; MUID:91103879; PMID:2271120  
A/Accession: B30412  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-93 <BLU>  
A/Cross-references: GB:M24110; GB:M32338; NID:G182848; PIDN:AAA35859.1; PID:G182849  
R/Irving, S.G.; Zipfel, P.F.; Balke, J.; McBride, O.W.; Morton, C.C.; Burd, P.R.; Siebe Nucleic Acids Res. 18, 3261-3270, 1990  
A/Title: Two inflammatory mediator cytokine genes are closely linked and variably ampli A/Reference number: S10157; MUID:90287702; PMID:1972563  
A/Accession: S10157  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-93 <IRV>  
A/Cross-references: EMBL:X52149; NID:G34750; PIDN:CAA36397.1; PID:G296666  
C/Comment: This protein is a member of a "small inducible" or "activation specific" gen C/Genetics:  
A/Gene: GDB:SCV4  
A/Cross-references: GDB:120369; OMIM:182284  
A/Map position: 17q11-17q21  
A/Introns: 26/1; 64/2  
C/Superfamily: macrophage inflammatory protein  
C/Keywords: cytokine  
F/1-22/Domain: signal sequence #status predicted <SIG>  
F/23-93/Product: LD78-beta protein #status predicted <MAT>  
Query Match 52.8%; Score 252.5; DB 2; Length 93;  
Best Local Similarity 47.8%; Pred. No. 1.9e-20;  
Matches 44; Conservative 25; Mismatches 22; Indels 1; Gaps 1;  
Qy 1 MKVSAARLAVILIALCAPASASPYSDT-TTPCCPAYIARPLPRAHIKEYFTYSGKCSN 59  
Db 1 MQVSTALAVLLCTWALCNQVLSAPLAADTPTACCSYTSRQIPQNFADYFETSSQCSK 60  
Qy 60 PAVVFTVRNQRQVCANPEKKVREYINLSLEMS 91  
Db 61 PSVIFLTKGRQVCADPSEWQVYVSDLELS 92  
RESULT 5  
A30574  
macrophage inflammatory protein 1-alpha precursor - human  
N/Alternate names: LD78-alpha protein precursor; lymphocyte tumor promoter-induced prot tivation protein 1  
C/Species: Homo sapiens (man)  
C/Date: 03-Aug-1992 #sequence\_revision 03-Aug-1992 #text\_change 21-Jul-2000





crophage inflammatory protein-1-alpha precursor - mouse  
 Alternate names: heparin-binding chemotaxis protein; IL25B protein; SCI/MIP-1a; SIS a  
 Species: Mus musculus (house mouse)  
 Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 16-Jul-1999  
 Accession: S11685; A32393; S04533; A53885; A30552; PS0303; A27596; I56104  
 Grove, M.; Lowe, S.; Graham, G.; Pragnell, I.; Plumb, M.  
 Citec Acids Res. 18, 5561, 1990  
 Title: Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammatory  
 protein-1 (IL-1) gene  
 Reference number: S11685; MUID:91016858; PMID:2216738  
 Accession: S11685  
 Molecule type: DNA  
 Residues: 1-92 <GRO>  
 Cross-references: EMBL:X53372; NID:G54062; PIDN:CAA37452.1; PID:G297531  
 Note: the authors' translation of the nucleotide sequence differs at several positions  
 Kwon, B.S.; Weissman, S.M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
 Title: cDNA sequence of two inducible T-cell genes.  
 Reference number: A32393; MUID:89184547; PMID:2784565  
 Accession: A32393  
 Molecule type: mRNA  
 Residues: 1-92 <KNO>  
 Cross-references: GB:J04491; NID:G201524; PIDN:AAA40304.1; PID:G201525  
 Davatellis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.; C  
 Exp. Med. 167, 1939-1944, 1988  
 Title: Cloning and characterization of a cDNA for murine macrophage inflammatory prote  
 Reference number: S04533; MUID:88258380; PMID:3290382  
 Accession: S04533  
 Molecule type: mRNA  
 Residues: 1-48, 'E', 'V', '90', 'I', '92 <DA2>  
 Cross-references: EMBL:X12531  
 Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue 9  
 Note: the sequence has been corrected in reference A53885  
 Davatellis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.; C  
 Exp. Med. 170, 2189, 1989  
 Reference number: A53885  
 Contents: erratum  
 Accession: A53885  
 Molecule type: mRNA  
 Residues: 1-92 <DAY>  
 Cross-references: EMBL:X12531; NID:G53122; PIDN:CAA31047.1; PID:G53123  
 Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
 Immunol. 142, 679-687, 1989  
 Title: A family of small inducible proteins secreted by leukocytes are members of a ne  
 of various activation processes.  
 Reference number: A30552; MUID:89093958; PMID:2521353  
 Accession: A30552  
 Molecule type: mRNA  
 Residues: 1-21, 'L', '23-61, 'A', '63-92 <BRO>  
 Cross-references: GB:M23447; NID:G533240; PIDN:AAA40146.1; PID:G533241  
 Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatellis, G.; Wolpe, S.D.; Ma  
 Exp. Med. 168, 2251-2259, 1988  
 Title: Resolution of the two components of macrophage inflammatory protein 1, and clon  
 Reference number: J10088; MUID:89067830; PMID:3058856  
 Accession: PS0303  
 Molecule type: protein  
 Residues: 24-33, 'XX', '36-54 <SHE>  
 Wolpe, S.D.; Davatellis, G.; Sherry, B.; Beutler, B.; Hesse, D.G.; Nguyen, H.T.; Moldaw  
 Exp. Med. 167, 570-581, 1988  
 Title: Macrophages secrete a novel heparin-binding protein with inflammatory and neut  
 Reference number: A27596; MUID:88154745; PMID:3279154  
 Accession: A27596  
 Molecule type: protein  
 Residues: 24-33, 'XX', '36-42 <WOL>  
 Note: 26-Met, 30-Pro, and 39-Thr were also found  
 Widmer, U.; Yang, Z.; van Deventer, S.; Manogue, K.R.; Sherry, B.; Cerami, A.  
 Immunol. 146, 4031-4040, 1991  
 Title: Genomic structure of murine macrophage inflammatory protein-1-alpha and conserv  
 Reference number: I56104; MUID:91237116; PMID:2033269  
 Accession: I56104  
 Status: preliminary; translated from GB/EMBL/DBJ  
 Molecule type: DNA  
 Residues: 1-92 <RES>  
 Cross-references: GB:M73061; NID:G199694; PIDN:AAA39707.1; PID:G199695

C:Comment: This protein is a monokine.

C:Genetics: 23/3; 26/1; 63/2  
 A:Introns: 23/3; 26/1; 63/2  
 C:Superfamily: macrophage inflammatory protein  
 A:Keywords: heparin binding  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-92/Product: macrophage inflammatory protein #status experimental <MAT>  
 Query Match 50.8%; Score 243; DB 2; Length 92;  
 Best Local Similarity 48.9%; Pred. No. 2, 1e-19;  
 Matches 45; Conservative 19; Mismatches 26; Indels 2; Gaps 2;  
 QY 1 MKVSAARLAVILATLALCAPASAFYSDDT-TPCCFAYIARPLPRAHIKEYFYTGKCSN 59  
 DB 1 MKVSTTALAVLLCTMTLCNQVFSAFYADTPTACCFSY-SRKIPRQFIVDYFETSSLCQ 59  
 QY 60 PAVVVTFRKNEQVCANPEKWKVREYINSLEMS 91  
 DB 60 PCVIFLTRKRNQICADSKETWQYETDLELN 91  
 RESULT 9  
 A31767  
 macrophage inflammatory protein 1-beta precursor [validated] - human  
 N:Alternate names: cytokine HC21; G-26 protein; H400 homolog; lymphocyte activation ge  
 protein 2 (Act-2); T-cell activation protein gamma  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Jun-1990 #sequence\_revision 29-May-1998 #text\_change 15-Sep-2000  
 C:Accession: JH0319; A40978; A31767; B30574; B45817; D30552  
 R:Baikeras, E.; Roman-Roman, S.; Jitsukawa, S.; Genevee, C.; Viegas-Pegu  
 Mol. Immunol. 27, 1091-1102, 1990  
 A:Title: Cloning and expression of a lymphocyte activation gene (LAG-1).  
 A:Reference number: JH0319; MUID:91061800; PMID:2247088  
 A:Accession: JH0319  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-92 <BAI>  
 A:Cross-references: GB:X53682; NID:G34217; PIDN:CAA37723.1; PID:G34218  
 A:Experimental source: natural killer cell, strain CD3-CD24, FS, 5L1IE5  
 R:Napolitano, M.; Modi, W.S.; Cevario, S.J.; Gnarr, J.R.; Seanez, H.N.; Leonard, W.J  
 J. Biol. Chem. 266, 17531-17536, 1991  
 A:Title: The gene encoding the Act-2 cytokine. Genomic structure, HTLV-1/tax responsiv  
 A:Reference number: A40978; MUID:91373378; PMID:1894635  
 A:Accession: A40978  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'S', '16-69, 'G', '71-92 <NAP>  
 A:Cross-references: GB:M69201; NID:G178021  
 A:Note: 15-Ala was also found  
 R:Ripes, M.A.; Napolitano, M.; Jeang, K.T.; Chang, N.T.; Leonard, W.J.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 9704-9708, 1988  
 A:Title: Identification, cloning, and characterization of an immune activation gene.  
 A:Reference number: A31767; MUID:89071764; PMID:2462251  
 A:Accession: A31767  
 A:Molecule type: mRNA  
 A:Residues: 1-92 <LIP>  
 A:Cross-references: GB:J04130; NID:G178017; PIDN:AAA51576.1; PID:G178018  
 R:Chang, H.C.; Reinherz, E.L.  
 Eur. J. Immunol. 19, 1045-1051, 1989  
 A:Title: Isolation and characterization of a cDNA encoding a putative cytokine which i  
 A:Reference number: A37411; MUID:89325421; PMID:2568930  
 A:Accession: A37411  
 A:Molecule type: mRNA  
 A:Residues: 1-92 <CHA>  
 A:Cross-references: GB:X16166; NID:G32035; PIDN:CAA34291.1; PID:G32036  
 R:Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.  
 J. Immunol. 142, 1582-1590, 1989  
 A:Title: Mitogenic activation of human T cells induces two closely related genes which  
 A:Reference number: A30574; MUID:89140347; PMID:2521882  
 A:Accession: B30574  
 A:Molecule type: mRNA  
 A:Residues: 1-19, 'L', '21-92 <ZIP>  
 A:Cross-references: GB:M25316; NID:G602454; PIDN:AAA57256.1; PID:G602455  
 R:Miller, M.D.; Hata, S.; Malefyt, R.D.W.; Krangel, M.S.

Immunol. 143, 2907-2916, 1989

Title: A novel polypeptide secreted by activated human T lymphocytes.

Reference number: A45817; MUID: 90038522; PMID: 2809212

Accession: B45817

Molecule type: mRNA

Residues: 7-55, 'I', 57-79, 'T', 81-92 <MIL>

Cross-references: GB:M57503; NID:G339726; PIDN:AAA36752.1; PID:G339727

Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.

Immunol. 142, 679-687, 1989

Title: A family of small inducible proteins secreted by leukocytes are members of a new

of various activation processes.

Reference number: A30552; MUID: 89093958; PMID: 2521353

Accession: D30552

Molecule type: mRNA

Residues: 1-39, 'REASS', 46-92 <BRO>

Cross-references: GB:M23502; NID:G533212; PIDN:AAA36656.1; PID:G533213

Clare, G.M.; Lodi, P.J.; Garrett, D.S.; Gronenborn, A.M.

mitted to the Brookhaven Protein Data Bank, January 1994

Reference number: A32206; PDB:1HUM

Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue

Comment: This protein is secreted by activated lymphocytes and monocytes. It is bound

Genetics:

Gene: GDB:LAG1

Cross-references: GDB:127451; OMIM:153335

Map position: 17q21-17q21

Introns: 26/1, 64/2

Superfamily: macrophage inflammatory protein

Keywords: chemotaxis; cytokine; inflammation

1-23/Domain: signal sequence #status predicted <SIG>

24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>

34-58,35-74/Disulfide bonds: #status experimental

Query Match 50.7%; Score 242.5; DB 1; Length 92;

Best Local Similarity 45.7%; Pred No. 2,3e-19;

Matches 42; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

1 MKVSAARLAVILIALCAPASASYSD-TTPCCFAYIARPLPRAHIKEY-FYTSKGCSN 59

1 MKLCVTLSLLMLVAAFCSPLASPMGSDPTACCFSTARKLPENFVDYETSSLCSQ 60

60 PAWVFVTKRQVNCANPEKKVREYINSLEMS 91

61 PAWVFQTKRQVNCADPSESQVQEVVDLEIN 92

ISULT 10

4912

taxin precursor - human

Species: Homo sapiens (man)

Date: 01-Nov-1995 #sequence\_revision 01-Nov-1996 #text\_change 20-Jun-2000

Accession: JG4912

Barcel, J.; Schlueter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroeder, B.

chem. Biophys. Res. Commun. 225, 1045-1051, 1996

Title: Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, a

Reference number: JG4912; MUID: 96374440; PMID: 8780731

Accession: JG4912

Status: preliminary

Molecule type: mRNA

Residues: 1-97 <BAR>

Cross-references: EMBL:275668; NID:G1531982; PIDN:CAA99997.1; PID:G1531983

Experimental source: dermal fibroblast

Comment: This protein has eosinophil specific chemotactic activity.

Superfamily: macrophage inflammatory protein

Keywords: fibroblast

1-18/Domain: signal sequence #status predicted <SIG>

19-97/Product: eotaxin #status predicted <MAT>

Query Match 35.1%; Score 168; DB 2; Length 97;

Best Local Similarity 41.1%; Pred. No. 3,2e-11;

Matches 37; Conservative 16; Mismatches 35; Indels 2; Gaps 2;

1 MKVSAARLAVILIALCAPASASYSDTTPCCFAYIARPLPRAHIKEY-FYTSKGCSN 59

Search completed: December 16, 2003, 15:40:57  
Job time : 13.4262 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

on: December 16, 2003, 15:36:20 ; Search time 10.4426 Seconds  
(without alignments)  
403.804 Million cell updates/sec

le: US-09-920-137A-8

fect score: 478

quence: 1 MKVSAARLAVILIALCAP.....VCANPEKKWVREYINSLEMS 91

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 127863 seqs, 47026705 residues

al number of hits satisfying chosen parameters: 127863

imum DB seq length: 0

cimum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

ult No.	Score	Query Match	Length	DB	ID	Description
1	472	98.7	91	1	SY05_HUMAN	P13501 homo sapien
2	416	87.0	91	1	SY05_CAVPO	P97272 cavia porce
3	404	84.5	91	1	SY05_BOVIN	O97919 bos taurus
4	393	82.2	91	1	SY05_MOUSE	P30882 mus musculus
5	383.5	80.2	92	1	SY05_RAT	P50231 rattus norv
6	372	77.8	91	1	SY05_SIGHI	Q91211 sigmodon hi
7	254.5	53.2	92	1	SY04_RABIT	P46632 coryctolagus
8	252.5	52.8	93	1	SY3L_HUMAN	P16619 homo sapien
9	251.5	52.6	90	1	SY04_CHICK	Q90826 gallus gall
10	248	51.9	92	1	SY03_HUMAN	P10147 homo sapien
11	248	51.9	92	1	SY03_RAT	P50229 rattus norv
12	245.5	51.4	92	1	SY04_MOUSE	P14097 mus musculus
13	243	50.8	92	1	SY03_MOUSE	P10855 mus musculus
14	242.5	50.7	92	1	SY04_HUMAN	P13236 h small ind
15	228.5	47.8	92	1	SY04_RAT	P50230 rattus norv
16	218	45.6	50	1	SY05_PIG	Q29288 sus scrofa
17	186	38.9	93	1	SV14_HUMAN	Q16627 homo sapien
18	182.5	38.2	89	1	SV18_HUMAN	P52774 h small ind
19	178.5	37.3	92	1	SY22_MOUSE	O88430 mus musculus
20	175	36.6	97	1	EOTA_HUMAN	P13671 homo sapien
21	174.5	36.5	94	1	SY26_HUMAN	P91258 homo sapien
22	167	34.9	99	1	SY07_HUMAN	P80098 homo sapien
23	165.5	34.6	120	1	SY23_HUMAN	P55773 homo sapien
24	162	33.9	120	1	SY02_CAVPO	Q08782 cavia porce
25	159.5	33.4	98	1	SV13_HUMAN	Q99616 homo sapien
26	158	33.1	113	1	SV15_HUMAN	Q18663 homo sapien
27	157.5	32.9	120	1	SV16_HUMAN	Q15467 h small ind
28	156	32.6	97	1	SY07_RAT	Q9GXY8 rattus norv
29	156	32.6	99	1	SY08_HUMAN	P80075 homo sapien
30	156	32.6	148	1	SV02_RAT	P14844 rattus norv
31	155	32.4	94	1	VM12_KSHV	Q98157 kaposi's sa
32	154	32.2	97	1	EOTA_RAT	P97545 rattus norv
33	152	31.8	97	1	SY07_MOUSE	Q03366 mus musculus

#### ALIGNMENTS

##### RESULT 1

ID	SY05_HUMAN	STANDARD;	PRT;	91 AA.
AC	P13501; O43646; Q9NYA2;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DE	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Small inducible cytokine A5 precursor (CC15)			
DE	protein) (SIS-delta) (T cell-specific protein P228) (TCp228).			
GN	CC15 OR SCYAS			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98285659; PubMed=2456327;			
RA	Schall T.J., Jongstra J., Dyer B.J., Jorgensen J., Clayberger C.,			
RA	Davis M.M., Krensky A.M.;			
RT	"A human T cell-specific molecule is a member of a new gene family."			
RL	J. Immunol. 141:1018-1025(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Jang J.S., Kim B.E.;			
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99228475; PubMed=10213461;			
RA	Nomiyama H., Fukuda S., Iio M., Tanase S., Miura R., Yoshie O.;			
RT	"Organization of the chemokine gene cluster on human chromosome			
RT	17q11.2 containing the genes for CC chemokine MIP-1, HCC-2, LEC, and			
RT	RANTES."			
RL	J. Interferon Cytokine Res. 19:227-234(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Zeng Q.P., Yang R.Y., Fu L.C.;			
RT	"The complete sequence of human beta-chemokine RANTES mRNA."			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=23388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Raha S.S., Loquellano N.A., Toshiyuki S., Carninci P., Prange C.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			

P42831 sus scrofa  
O00626 homo sapien  
P82943 bos taurus  
Q09141 bos taurus  
P48298 mus musculus  
P10148 mus musculus  
P28291 bos taurus  
P52203 canis fami  
P49873 sus scrofa  
P80325 cavia porce  
P13500 homo sapien  
Q9MYH4 macaca fasc

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [6]  
 SEQUENCE OF 49-56; 71-79 AND 83-91, AND FUNCTION.  
 MEDLINE=96106406; PubMed=8525373;  
 Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C., Lusso P.;  
 "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells";  
 Science 270:1811-1815(1995).  
 [7]

STRUCTURE BY NMR.  
 MEDLINE=95352612; PubMed=7542919;  
 Chung C.-W., Cooke R.M., Proudfoot A.E.I., Wells T.N.C.;  
 "The three-dimensional solution structure of RANTES";  
 Biochemistry 34:9307-9314(1995).  
 [8]  
 STRUCTURE BY NMR.  
 MEDLINE=95244456; PubMed=7537088;  
 Skelton N.J., Aspiras F., Ogez J., Schall T.J.;  
 "Proton NMR assignments and solution conformation of RANTES, a chemokine of the C-C type";  
 Biochemistry 34:5329-5342(1995).  
 [9]

SYNTHESIS, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 MEDLINE=99111238; PubMed=9889151;  
 Wilken J., Hoover D., Thompson D.A., Barlow P.N., McSparron H., Picard L., Wlodawer A., Lubkowski J., Kent S.B.;  
 "Total chemical synthesis and high-resolution crystal structure of the potent anti-HIV protein AOP-RANTES";  
 Chem. Biol. 6:43-51(1999).  
 [10]

X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 Hoover D.M., Shaw J., Gryczynski Z., Proudfoot A.E.I., Wells T.N.C., Lubkowski J.;  
 "The crystal structure of Met-RANTES: comparison with native RANTES and AOP-RANTES";  
 Protein. Pept. Lett. 7:73-82(2000).

-1- FUNCTION: CHemoattractant for blood monocytes, memory T helper cells and eosinophils. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.

-1- INDUCTION: By mitogens.  
 -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).

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EMBL; M21121; AAA36725.1; -;  
 EMBL; AF043341; AAC03541.1; -;  
 EMBL; AF088219; AAC63331.1; -;  
 EMBL; AF266753; AAF73070.1; -;  
 EMBL; BC008600; AAH06600.1; -;  
 PIR; A28815; A28815.  
 PDB; 1HRJ; 14-OCT-96.  
 PDB; 1RTN; 03-JUN-95.  
 PDB; 1RTQ; 03-JUN-95.  
 PDB; 1B3A; 23-APR-99.

DR PDB; 1EQT; 19-APR-00.  
 DR Genew; HGNC:10632; CCL5.  
 DR MIM; 187011; -;  
 DR GO; GO:0003800; F:antiviral response protein activity; TAS.  
 DR GO; GO:0008009; F:chemokine activity; TAS.  
 DR GO; GO:0006874; P:calcium ion homeostasis; TAS.  
 DR GO; GO:0007155; P:cell adhesion; TAS.  
 DR GO; GO:0006928; P:cell motility; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006968; P:cellular defense response; TAS.  
 DR GO; GO:0006935; P:chemotaxis; TAS.  
 DR GO; GO:0006887; P:exocytosis; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR GO; GO:0006979; P:response to oxidative stress; TAS.  
 DR GO; GO:0006615; P:response to viruses; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR000827; CC\_chemokine\_sml.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCV; 1.  
 DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 DR Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response;  
 KW 3D-structure. 1 23  
 FT SIGNAL 24 91 SMALL INDUCIBLE CYTOKINE A5.  
 FT CHAIN 33 57  
 FT DISULFID 34 73  
 FT CONFLICT 7 7 A -> R (IN REF. 1 AND 4).  
 FT CONFLICT 14 14 A -> V (IN REF. 4).  
 FT STRAND 30 33  
 FT HELIX 44 46  
 FT STRAND 47 52  
 FT TURN 55 56  
 FT STRAND 62 66  
 FT TURN 67 68  
 FT TURN 71 74  
 FT STRAND 76 77  
 FT TURN 79 91  
 FT HELIX 79 91  
 SQ SEQUENCE 91 AA; 9990 MW; PBOBFAF9A87C620F CRC64;

Query Match 98.7%; Score 472; DB 1; Length 91;  
 Best Local Similarity 98.9%; Pred. No. 7.3e-46;  
 Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATALCAPASAPSYSDTTPCCFAVIARPLPRAHIKEYFTYTSKCSNP 60  
 DB 1 MKVSAARLAVILIATALCAPASAPSYSDTTPCCFAVIARPLPRAHIKEYFTYTSKCSNP 60  
 QY 61 AVVFVTRKNQVCANPEKKVREYINSLEMS 91  
 DB 61 AVVFVTRKNQVCANPEKKVREYINSLEMS 91

## RESULT 2

SY05 CAVPO STANDARD; PRT; 91 AA.  
 ID SY05 CAVPO STANDARD; PRT; 91 AA.  
 AC P97272; O09076;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta).  
 DE CCL5 OR SCVAs.  
 GN Cavia porcellus (Guinea pig).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_taxid=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dunkin-Hartley;  
 RA Campbell E.M., Proudfoot A.E.I., Yoshimura T., Allet B.,  
 RA Wells T.N.C., White A.M., Westwick J., Watson M.L.;  
 RA Submitted (NOV-1996) to the ENBL/GenBank/DBJ databases.  
 RL

```

[2]
SEQUENCE FROM N.A.
TISSUE=Lung;
Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A.,
Yamaguchi K., Kanazawa M.;
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
-----
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or send an email to license@isb-sib.ch).
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EMBL; U77037; AAC53293.1; -.
HSP; P13501; 1RTN.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; T-cell; Signal; Inflammatory response.
SIGNAL 1 23 POTENTIAL.
CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
DISULFID 33 57 BY SIMILARITY.
DISULFID 34 73 BY SIMILARITY.
SEQUENCE 91 AA; 1008 MW; 7FGA31B751237DB9 CRC64;

Query Match 87.0%; Score 416; DB 1; Length 91;
Best Local Similarity 86.8%; Pred. No. 1.3e-39;
Matches 79; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFYTSKGKSNP 60
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1 MKVSAARLAVILTTAALCVAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFYTSKGKSNL 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

61 AVFVTRKNQVCANPEKKWREYINSLEMS 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 AVFVTRKNQVCANPEKKWREYINSLEMS 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

ULT 3
5 BOVIN
-!- SY05 BOVIN STANDARD; PRT; 91 AA.
O97319;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
protein) (SIS-delta).
CCL5 OR SCYAS.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
TISSUE=Intestine;
Aust G., Thamm B., Rost A.K.;
"Cloning of Bos taurus RANTES mRNA.";
Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
-----
EMBL; AJ007043; CAA07430.1; -.
HSP; P13501; 1RTN.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; T-cell; Signal; Inflammatory response.
SIGNAL 1 23 POTENTIAL.
CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
DISULFID 33 57 BY SIMILARITY.
DISULFID 34 73 BY SIMILARITY.
SEQUENCE 91 AA; 10073 MW; 660DD38E015B0735 CRC64;

Query Match 84.5%; Score 404; DB 1; Length 91;
Best Local Similarity 80.2%; Pred. No. 2.7e-38;
Matches 73; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFYTSKGKSNP 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MKVSAATAFVALLMAAALCAPASAPSYSDTTCCCFAYISRPILRTHVQVYFYTSKCSMA 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
SY05 MOUSE
ID -SY05 MOUSE STANDARD; PRT; 91 AA.
AC P30832;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
protein) (SIS-delta) (MuRantes).
GN CCL5 OR SCYAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92277990; PubMed=1375672;
RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
RA Krensky A.M., Neilson E.G.;
RT "Isolation and characterization of cDNA from renal tubular epithelium
encoding murine Rantes.";
RL Kidney Int. 41:220-225(1992).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92289805; PubMed=1376260;
RA Schall T.J., Simpson N.J., Mak J.Y.;
RT "Molecular cloning and expression of the murine RANTES cytokine:
structural and functional conservation between mouse and man.";
RL Eur. J. Immunol. 22:1477-1481(1992).
[3]
RP SEQUENCE FROM N.A.
RX STRAIN=NIH Swiss; PubMed=7507961;
RL Danoff T.M., Talley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;

```

"Cloning, genomic organization, and chromosomal localization of the scv5a gene encoding the murine chemokine RANTES.";  
J. Immunol. 152:1182-1189(1994).  
[4]  
SEQUENCE FROM N.A.  
STRAIN=BAUB/c;  
MEDLINE=94217689; PubMed=7513046;  
Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,  
Paznekas W.A.;  
"Definition of a lipopolysaccharide-responsive element in the 5'-  
flanking regions of MuRantes and crg-2";  
Mol. Cell. Biol. 14:2914-2925(1994).  
[5]  
SEQUENCE FROM N.A.  
STRAIN=B10.S/J, BALB/CJ, DBA/2J, NOD/LTJ, and SJL/J; TISSUE=Spleen;  
MEDLINE=99370037; PubMed=10438970;  
Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
Blankenhorn E.P.;  
"Sequence polymorphisms in the chemokines Scv1 (TCA-3), Scv2  
(monocyte chemoattractant protein (MCP)-1), and Scv12 (MCP-5) are  
candidates for eae7, a locus controlling susceptibility to monophasic  
remitting/non-relapsing experimental allergic encephalomyelitis";  
J. Immunol. 163:2262-2266(1999).  
[6]  
SEQUENCE FROM N.A.  
STRAIN=129/Sv;  
Nomiya H.;  
"Organization of the mouse CC chemokine cluster containing the genes  
for C10, MRP-2 and RANTES";  
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
[7]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Pancreas;  
PubMed=12466851;  
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,  
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,  
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
Verardo R., Wagner L., Wählstedt C., Wang Y., Watanabe Y., Wells C.,  
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,  
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
Birney E., Hayashizaki Y.;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs";  
Nature 420:563-573(2002).  
[8]  
SEQUENCE FROM N.A.  
TISSUE=Mammary gland;  
PubMed=12477932;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Rasak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Faneay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RL  
CC -!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER  
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
CC BASOPHILS AND ACTIVATES EOSINOPHILS.  
CC  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC  
CC -!- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.  
CC  
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
CC C-C) (CHEMOKINE CC).  
CC  
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CC  
CC EMBL; M77747; AAA40029.1; -;  
CC EMBL; S37648; AAB22330.1; -;  
CC EMBL; U02298; AAA18302.1; -;  
CC EMBL; X70675; CAA50011.1; -;  
CC EMBL; AF065944; AAC17511.1; -;  
CC EMBL; AF065945; AAC17512.1; -;  
CC EMBL; AF065946; AAC17513.1; -;  
CC EMBL; AF065947; AAC17514.1; -;  
CC EMBL; AF128187; AAF22528.1; -;  
CC EMBL; AB051897; BAB18731.1; -;  
CC EMBL; AK003101; BAB22566.1; -;  
CC EMBL; BC033508; AAB33508.1; -;  
CC PIR; I48875; A46539.  
CC HSP; P13501; IRTN.  
CC MGD; MGI:98262; Ccl5.  
CC InterPro; IPR000827; CC\_chemokine\_sml.  
CC InterPro; IPR001811; Chemokine\_il8.  
CC Pfam; PF00048; IL8; 1.  
CC SMART; SM00159; SCY; 1.  
CC PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.  
FT DISULFID 33 57 BY SIMILARITY.  
FT DISULFID 34 73 BY SIMILARITY.  
FT CONFLICT 19 19 T -> A (IN REF. 2).  
FT CONFLICT 41 41 A -> E (IN REF. 1).  
SQ SEQUENCE 91 AA; 10071 MW; 5DFD66F4684FE1C8 CRC64;  
  
Query Match 82.2%; Score 393; DB 1; Length 91;  
Best Local Similarity 79.1%; Pred. No. 4.6e-37;  
Matches 72; Conservative 7; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 MKVSAARLAVILIALCAPASAPSYSDTTPCCFAYIARPLPAHKEYFTYSGKCSNP 60  
DB 1 MKISAAALITLITAAALCTAPASPSGSDTTPCCFAYLSIALPRAHVKEYFTYSGKCSNL 60  
  
QY 61 AVFVTRNRQVCANPEKQWVREYINLEMS 91  
DB 61 AVFVTRNRQVCANPEKQWVREYINLEMS 91  
  
RESULT 5



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OC Sigmomon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Bianco J.C., Pietneva L.M., Prince G.A.;
RT "Sigmomon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF421391; AAL16932.1; -
CC Inter-Pro: IPR000827; CC chemkine sm1.
CC DR Inter-Pro: IPR001811; Chemokine_I18.
CC DR Pfam: PF000048; IL8; 1.
CC DR SMART: SM00199; SCY; 1.
CC DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC DR Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
CC KW SIGNAL 1 23 POTENTIAL.
CC FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
CC FT DISULFID 33 57 BY SIMILARITY.
CC FT DISULFID 34 73 BY SIMILARITY.
CC SEQUENCE 91 AA; 10082 MW; D0D6EAEABE4242FF CRC64;
Query Match 77.8%; Score 372; DB 1; Length 91;
Best Local Similarity 75.6%; Pred. No.1e-34;
Matches 68; Conservative 11; Mismatches 11; Indels 0; Gaps 0;
QY 1 MKVSAARLAIVLIALTALCAPASPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60
DQ 1 MKISAIVLTWLAASLCAPASPSNGSDTTPCCPAYLSAVLPRAHVKEYFTSSKCSNF 60
QY 61 AVVFVTRNRQVCANPEKKWREYINSLEM 90
DB 61 AVVFVTRNRQVCANPEKKWQVEYINYLEL 90
RESULT 7
ID SY04_RABIT STANDARD; PRT; 92 AA.
AC P46632;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
DE protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).
DE CCL4 OR SCV44.
GN Oryctolagus cuniculus (Rabbit)
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=New Zealand white;
RX MEDLINE=94198229; PubMed=6148323;
RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156(1994).
CC -1- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES
CC (BY SIMILARITY).
CC -1- SUBUNIT: Homodimer (By similarity).

```

MEDLINE=90287155; PubMed=1694014;  
 Nakao M., Noniyama H., Shimada K.;  
 "Structures of human genes coding for cytokine LD78 and their  
 expression."; Mol. Cell. Biol. 10:3646-3658 (1990).  
 [4]  
 SEQUENCE FROM N.A.  
 TISSUE=B-Cell, Pancreas, and Spleen;  
 MEDLINE=2338257; PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Schuler G.D.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Diatchenko M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,  
 Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 -!- SUBCELLULAR LOCATION: Secreted.  
 -!- SIMILARITY: BELONGS TO THE INTERFERON BETA FAMILY (SMALL CYTOKINE  
 C-CL) (CHEMOKINE CC). STRONG, TO SCY43.  
 ---  
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 EMBL; X52149; CAA36397.1; -;  
 EMBL; M24110; AAA35659.1; -;  
 EMBL; D90145; BAA14173; -;  
 EMBL; BC007783; AAH07783.1; -;  
 EMBL; BC027888; AAH27888.1; -;  
 PIR; B35673; B35673.  
 HSSP; P12336; 1HUM.  
 Genew; HGNC:10628; CCL3L1.  
 MIM; 601395; -;  
 GO; GO:0005576; C:extracellular; NAS.  
 GO; GO:0008009; F:chemokine activity; NAS.  
 GO; GO:0008935; P:chemotaxis; NAS.  
 GO; GO:0008594; P:inflammatory response; TAS.  
 GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
 InterPro; IPR000827; CC.Chemokine\_sm1.  
 InterPro; IPR001811; Chemokine\_IL8.  
 Pfam; PF00048; IL8; 1.  
 SMART; SM00199; SCY; 1.  
 PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 Cytokine; Chemotaxis; Signal.  
 SIGNAL  
 1 23  
 FT CHAIN 34 58  
 FT DISULFID 24 93  
 FT DISULFID 35 74  
 FT DISULFID 91 91  
 FT CONFICT 91 91  
 SEQUENCE 93 AA; 10161 MW; A7A79E774006D61E CRC64;  
 Query Match 52.8%; Score 252.5; DB 1; Length 93;  
 Best Local Similarity 47.8%; Pred. No. 21e-22;  
 Matches 44; Conservative 25; Mismatches 21; Indels 1; Gaps 1;  
 QY 1 MKVSAARLAVILIAVIALCAPASAPSYSDT-TPCCFAYIARPLPRAHIKEYFTYSGKSN 59

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1  MQVSTAAVLCTWALCNQVLSAPLAADPTACCPSTYTSRQIPONFIADYPETSSQSK 60
60  PAIVFVTRKGRQVCANPEKKWREYINSLEMS 91
61  PSVIFLTGRQVCADPSEEWQXVYSDLELS 92

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Q9026; Q910C9;  
01-NOV-1997 (Rel. 35, Created)  
28-FEB-2003 (Rel. 41, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Small inducible cytokine A4 homolog precursor (Macrophage inflammatory protein 1-beta homolog).  
CCL4 OR SCYA4  
Gallus gallus (Chicken).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
Gallus.  
NCBI\_TaxID=9031;  
[1]\_  
SEQUENCE FROM N. A.  
TISUE=Bone marrow;  
MEDLINE=93569710; PubMed=7642115;  
Petrenko O., Ischenko I., Enrietto P.J.;  
"Isolation of a cDNA encoding a novel chicken chemokine homologous to mammalian macrophage inflammatory protein-1 beta.";  
Gene 160:305-306(1995).  
[2]  
SEQUENCE FROM N. A.  
Hughes S.M., Bumstead N.;  
"Mapping of the gene encoding the chicken homologue of the mammalian chemokine SCYA4.";  
Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE OF 14-90 FROM N. A.  
Petrenko O., Enrietto P.J.;  
Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES (BY SIMILARITY).  
-!- SUBUNIT: Homodimer (By similarity).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).  
  
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EMBL; L34553; AAA48747.1; .  
EMBL; AJ243034; CAB45103.1; .  
HSP; P13236; 1HUM.  
InterPro: IPR000827; CC chemkine sm1.  
InterPro: IPR001811; Chemokine\_IL8.  
Pfam: PF00048; IL8; 1  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; Signal.  
SIGNAL 1 21  
CHAIN 22 90  
DISULFD 32 56  
DISULFD 33 72  
CONFLICT 87 87  
SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;  
BY SIMILARITY.  
SMALL INDUCIBLE CYTOKINE A4 HOMOLOG.  
BY SIMILARITY.  
BY SIMILARITY.  
M -> L (IN REF. 1).  
SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;

Query Match



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R InterPro; IPR000827; CC_chemkine.sml.
R InterPro; IPR001811; Chemokine_IL8.
R Pfam; PF00048; IL8; 1.
R SMART; SM00199; SCY; 1.
R PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
W Cytokine; Chemotaxis; Inflammatory response; Signal; Heparin-binding.
T SIGNAL 1 23 SMALL INDUCIBLE CYTOKINE A3.
T CHAIN 24 92 BY SIMILARITY.
T DISULFID 34 57 BY SIMILARITY.
T DISULFID 35 73 BY SIMILARITY.
T CONFLICT 6 6 A -> T (IN REF. 2).
T CONFLICT 57 57 C -> W (IN REF. 2 AND 3).
Q SEQUENCE 92 AA; 10335 MW; 14E961C647P9A2EB CRC64;

Query Match 51.9%; Score 248; DB 1; Length 92;
Best Local Similarity 51.1%; Pred. No. 6.5e-21;
Matches 47; Conservative 18; Mismatches 25; Indels 2; Gaps 2;

Y 1 MKVSAARLAVILIALTALCAPASAPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSKCSN 59
b 1 MKVSTAALAVLLCTWALNWEVAFSGADTPTACCFSY-GRQIPKFIADYFETSSLSQ 59
Y 60 PAVFVTRKNQVCANPEKKVREYINSLEMS 91
b 60 PGVIFLTKRQICADPKETWQCEVITELN 91

RESULT 12
Y04_MOUSE
D SY04_MOUSE STANDARD; PRT; 92 AA.
C P14057;
I 01-JAN-1990 (Rel. 13, Created)
I 01-FEB-1996 (Rel. 33, Last sequence update)
I 15-SEP-2003 (Rel. 42, Last annotation update)
E Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
E protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2).
N CCL4 OR SCYA4 OR MIP-1B.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NCBI_TaxID=10090;
P [1]
P SEQUENCE FROM N.A.
X MEDLINE=89067930; PubMed=3058856;
A Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G.,
A Wolpe S.D., Masiarz F., Coit D., Cerami A.;
T "Resolution of the two components of macrophage inflammatory protein
T 1, and cloning and characterization of one of those components,
T macrophage inflammatory protein 1 beta.";
T J. Exp. Med. 168:2251-2259 (1988).
P [2]
P SEQUENCE FROM N.A.
X MEDLINE=89093958; PubMed=2521353;
A Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
T "A family of small inducible proteins secreted by leukocytes are
T members of a new superfamily that includes leukocyte and fibroblast-
T derived inflammatory agents, growth factors, and indicators of various
T activation processes.";
T J. Immunol. 142:679-687 (1989).
P [3]
P SEQUENCE FROM N.A.
C STRAIN=BA/2J; TISSUE=Liver;
A Daubersies P., Lepretre F., Bailleul B., Grove M., Pragnell I.,
A Plumb M.A.;
N Submitted (Oct-1991) to the EMBL/GenBank/DBJ databases.
P [4]
P SEQUENCE FROM N.A.
C STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;
X MEDLINE=59370037; PubMed=10438970;
A Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.P., Doerge R.W.,
A Blankenhorn E.P.;
I "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2
I (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are

```

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candidates for eae7, a locus controlling susceptibility to monophasic
remitting/nonrelapsing experimental allergic encephalomyelitis.";
J. Immunol. 163:2262-2266(1999).
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
-----
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or send an email to license@isb-sib.ch).
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EMBL; M35590; AAA39708.1; -
EMBL; X62502; CAA44364.1; -
EMBL; AF128218; AAF22559.1; -
EMBL; AF128219; AAF22560.1; -
PIR; C30552; C30552.
HSSP; P13236; IHUM.
MGD; MGI:98261; Ccl4.
InterPro; IPR000827; CC_chemkine.sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 23 SMALL INDUCIBLE CYTOKINE A4.
FT CHAIN 24 92 BY SIMILARITY.
FT DISULFID 34 58 BY SIMILARITY.
FT DISULFID 35 74 BY SIMILARITY.
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Best Local Similarity 45.7%; Pred. No. 1.2e-20;
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Db 61 PAVFVTRKNQVCANPEKKVREYINSLEMS 92

RESULT 13
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ID SY03_MOUSE STANDARD; PRT; 92 AA.
AC P10855; P14096;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
DE protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (Heparin-binding
DE chemotaxis protein) (I2G25B).
GN CCL3 OR SCYA3 OR MIP1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RX MEDLINE=88258380; PubMed=3290382;
RA Davatelis G., Tekamp-Olson P., Wolpe S.D., Herman K., Luedke C.,
RA Gallegos C., Coit D., Merryweather J., Cerami A.;
RT "Cloning and characterization of a cDNA for murine macrophage
RT inflammatory protein (MIP), a novel monokine with inflammatory and
RT chemokinetic properties.";

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J. Exp. Med. 167:1939-1944 (1988).  
 (2)  
 REVISIONS.  
 Davatellis G., Tekamp-Olson P., Wolpe S.D., Hermens K., Luedke C., Gallegos C., Coit D., Merryweather J., Cerami A.;  
 J. Exp. Med. 170:2189-2189 (1989).  
 (3)  
 SEQUENCE FROM N.A.  
 MEDLINE=89093958; PubMed=2521353;  
 Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;  
 "A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes."  
 J. Immunol. 142:679-687 (1989).  
 (4)  
 SEQUENCE FROM N.A.  
 STRAIN=DA/2J;  
 MEDLINE=91016858; PubMed=2216738;  
 Grove M., Lowe S., Graham G., Pragnell I., Plumb M.;  
 "Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammatory protein-1 alpha gene";  
 Nucleic Acids Res. 18:5561-5561 (1990).  
 (5)  
 SEQUENCE FROM N.A.  
 MEDLINE=89184547; PubMed=2784565;  
 Kwon B.S., Weissman S.M.;  
 "cDNA sequences of two inducible T-cell genes";  
 Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967 (1989).  
 (6)  
 SEQUENCE FROM N.A.  
 MEDLINE=91237116; PubMed=2033269;  
 Widner U., Yang Z., van Deventer S., Manogue K.R., Sherry B., Cerami A.;  
 "Genomic structure of murine macrophage inflammatory protein-1 alpha and conservation of potential regulatory sequences with a human homolog, LD78";  
 J. Immunol. 146:4031-4040 (1991).  
 (7)  
 SEQUENCE FROM N.A.  
 STRAIN=BALB/CJ, DBA/2J, NOD/LTY, SJL/J, and B10.S/J; TISSUE=Spleen;  
 MEDLINE=99370037; PubMed=10438970;  
 Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W., Blankenhorn E.P.;  
 "Sequence polymorphisms in the chemokines Sclay (TCA-3), Scya2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for eae7, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis";  
 J. Immunol. 163:2262-2266 (1999).  
 (8)  
 SEQUENCE OF 24-42.  
 MEDLINE=88154745; PubMed=3279154;  
 Wolpe S.D., Davatellis G., Sherry B., Beutler B., Hesse D.G., Nguyen H.T., Moldawer L.L., Nathan C.F., Lowry S.F., Cerami A.;  
 "Macrophages secrete a novel heparin-binding protein with inflammatory and neutrophil chemokinetic properties";  
 J. Exp. Med. 167:570-581 (1988).  
 (9)  
 FUNCTION: MONOKINE WITH INFLAMMATORY, PYROGENIC AND CHEMOKINETIC PROPERTIES. HAS A POTENT CHEMOTACTIC ACTIVITY FOR EOSINOPHILS. BINDING TO A HIGH-AFFINITY RECEPTOR ACTIVATES CALCIUM RELEASE IN NEUTROPHILS.  
 (10)  
 SUBCELLULAR LOCATION: Secreted.  
 (11)  
 TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, AND PANCREAS.  
 (12)  
 SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).  
 (13)  
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CC EMBL; M23447; AAA40146.1; -  
 DR EMBL; X12531; CAA31047.1; -  
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 DR EMBL; M73061; AAA39707.1; -  
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 DR EMBL; AF065942; AAC17509.1; -  
 DR EMBL; AF065943; AAC17510.1; -  
 DR PIR; S11685; A32393.  
 DR HSSP; P13236; IHUM.  
 DR MGD; MGI-98260; Cel3.  
 DR GO; GO:0008009; F:chemokine activity; IDA.  
 DR InterPro; IPR000827; CC\_chemokine\_sml.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.  
 FT SIGNAL 1 23 SMALL INDUCIBLE CYTOKINE A3.  
 FT CHAIN 24 92 BY SIMILARITY.  
 FT DISULFID 34 57 BY SIMILARITY.  
 FT DISULFID 35 73 BY SIMILARITY.  
 FT CONFLICT 22 22 F -> L (IN REF. 3).  
 FT CONFLICT 62 62 V -> A (IN REF. 3).  
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 AC P13236; F22617; Q13704;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Small inducible cytokine A4 precursor (CC14) (Macrophage inflammatory protein 1-beta) (MIP-1-beta) (T-cell activation protein 2) (ACT-2) (PRT 744) (H400) (SIS-gamma) (Lymphocyte activation gene-1 protein) (LAG-1) (HC21) (G-26 T lymphocyte-secreted protein).  
 DE CCL4 OR SCY44 OR MIP1B OR LAG1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89071764; PubMed=2462251;  
 RA Lipke M.A., Napolitano M., Jeang K.-T., Chang N.T., Leonard W.J.;  
 "Identification, cloning, and characterization of an immune activation gene";  
 Proc. Natl. Acad. Sci. U.S.A. 85:9704-9708 (1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89140347; PubMed=2521882;  
 RA Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;  
 "Mitogenic activation of human T cells induces two closely related genes which share structural similarities with a new family of secreted factors";  
 J. Immunol. 142:1582-1590 (1989).

[3] SEQUENCE FROM N.A.  
MEDLINE=89093959; PubMed=2521353;  
Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;  
"A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.";  
J. Immunol. 142:679-687(1989).  
[4] SEQUENCE FROM N.A.  
MEDLINE=91061800; PubMed=2247088;  
Baixeras E., Roman-Roman S., Jitsukawa S., Genevee C., Mechiche S., Viegas-Pequignot E., Hercend T., Triebel P.;  
"Cloning and expression of a lymphocyte activation gene (LAG-1).";  
Mol. Immunol. 27:1091-1102(1990).  
[5] SEQUENCE FROM N.A.  
TISSUE=T-cell;  
MEDLINE=89325421; PubMed=2568930;  
Chang H.C., Reihertz E.L.;  
"Isolation and characterization of a cDNA encoding a putative cytokine which is induced by stimulation via the CD2 structure on human T lymphocytes.";  
Eur. J. Immunol. 19:1045-1051(1989).  
[6] SEQUENCE FROM N.A.  
MEDLINE=91373378; PubMed=1894635;  
Napolitano M., Modi W.S., Cevario S.J., Gnarra J.R., Seunanez H.N., Leonard W.J.;  
"The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/Tax responsiveness of 5' upstream sequences, and chromosomal localization.";  
J. Biol. Chem. 266:17531-17536(1991).  
[7] SEQUENCE FROM N.A.  
Birren B., Fauman K., McKernan K., Nusbaum C., Richardson P., Lander E.;  
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
[8] SEQUENCE OF 6-92 FROM N.A.  
MEDLINE=90038522; PubMed=2809212;  
Miller M.D., Hata S., Waal Malefyt R., Krangel M.S.;  
"A novel polypeptide secreted by activated human T lymphocytes.";  
J. Immunol. 143:2907-2916(1989).  
[9] RECEPTOR INTERACTION.  
MEDLINE=98180363; PubMed=9521068;  
Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G., Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A., Napolitano M.;  
"Identification of the CC chemokines TARC and macrophage inflammatory protein-1 beta as novel functional ligands for the CCR8 receptor.";  
Eur. J. Immunol. 28:582-588(1998).  
[10] FUNCTION.  
MEDLINE=96106406; PubMed=8525373;  
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C., Lusso P.;  
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells.";  
Science 270:1811-1815(1995).  
[11] STRUCTURE BY NMR.  
MEDLINE=94182137; PubMed=8134838;  
Lodi P.J., Garrett D.S., Kucsewski J., Tsang M.L.S., Weatherbee J.A., Leonard W.J., Gronenborn A.M., Clore G.M.;  
"High-resolution solution structure of the beta chemokine hMIP-1 beta by multidimensional NMR.";  
Science 263:1762-1767(1994).  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES. BINDS TO CCR5 AND TO CCR8. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-BETA INDUCES A

CC DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2,  
CC AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- INDUCTION: By mitogens.  
CC -!- SIMILARITY: BELONGS TO THE INTERKINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).  
CC  
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CC  
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CC GO; GO:0005615; C:extracellular space; TAS.  
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CC GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . . ; TAS.  
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CC GO; GO:0007267; P:cell-cell signaling; TAS.  
CC GO; GO:0007163; P:establishment and/or maintenance of cell po. . . ; TAS.  
CC GO; GO:0006955; P:immune response; TAS.  
CC GO; GO:0006954; P:inflammatory response; TAS.  
CC GO; GO:0006915; P:response to viruses; TAS.  
CC GO; GO:0007165; P:signal transduction; TAS.  
CC GO; GO:0008166; P:viral replication; TAS.  
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CC SMART; SM00199; SCY; 1.  
CC PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.  
FT SIGNAL 1 23  
FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.  
FT DISULFID 34 58 BY SIMILARITY.  
FT DISULFID 35 74 BY SIMILARITY.  
FT CONFLICT 5 6 T -> C (IN REF. 7).  
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FT CONFLICT 40 45 ARKLPK -> REASS (IN REF. 3).  
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FT CONFLICT 80 80 S -> T (IN REF. 7 AND 8).  
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FT TURN 77 78  
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protein - protein search, using sw model

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(without alignments)  
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file: US-09-920-137A-8

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ximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriaph.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	406	84.9	91	6 Q8MKD0	Q8mkd0 equus caball
3	370	77.4	91	6 Q8HYQ0	Q8hyq0 canis famil
4	362.5	75.8	92	6 Q8SQ40	Q8sq40 felis silve
5	284.5	59.5	91	13 Q8QGS7	Q8qgs7 gallus gall
6	283	59.2	50	6 Q8HYN5	Q8hyn5 macaca mula
7	268.5	56.2	93	6 Q8SQ46	Q8sq46 bos taurus
8	252	52.7	92	6 Q8HYQ3	Q8hyq3 macaca mula
9	251.5	52.6	92	6 Q8HYQ2	Q8hyq2 macaca mula
10	248.5	52.0	90	13 Q9PWA6	Q9pwa6 gallus gall
11	247.5	51.8	92	11 Q91ZL0	Q91zl0 sigmodon hi
12	232	48.5	92	11 Q91Z65	Q91z65 sigmodon hi
13	230.5	48.2	92	4 Q8NH44	Q8nhw4 homo sapien
14	213	44.6	80	4 Q14745	Q14745 homo sapien
15	213	44.6	89	13 Q918E0	Q918e0 gallus gall
16	204	42.7	91	13 Q8QGS6	Q8qgs6 gallus gall

17	181	37.9	56	6 Q8HYN4	Q8hyn4 macaca mula
18	181	37.9	88	6 Q8HYP8	Q8hy p8 macaca mula
19	178.5	37.3	92	11 Q9QZU2	Q9qzu2 mus musculu
20	177.5	37.1	92	6 Q8MI76	Q8mi76 bos taurus
21	172.5	36.1	92	11 Q91ZHS	Q91zh5 rattus norv
22	171.5	35.9	81	11 Q9QZU1	Q9qzu1 rattus norv
23	161	33.7	97	6 Q8HXZ5	Q8hxz5 macaca mula
24	155	32.4	100	6 Q9TTQ4	Q9ttq4 equus cabal
25	154	32.2	95	12 Q981S8	Q981s8 kaposi's sa
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27	153	32.0	97	6 Q8MIT7	Q8mit7 macaca mula
28	153	32.0	99	6 Q8HYQ0	Q8hyq0 macaca mula
29	151.5	31.7	97	6 Q9TTS6	Q9tts6 bos taurus
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31	150	31.4	49	6 Q8HYN3	Q8hyn3 macaca mula
32	150	31.4	100	6 Q95MD5	Q95md5 bos taurus
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34	145.5	30.4	148	11 Q9QYD7	Q9qyd7 mus musculu
35	140.5	28.4	120	6 Q8HYP4	Q8hy p4 macaca mula
36	138	28.9	81	6 Q9TTQ2	Q9ttq2 equus cabal
37	138	28.9	91	13 Q8JIM5	Q8jim5 paralicthy
38	136	28.5	91	13 Q8AV56	Q8av56 paralicthy
39	134	28.0	91	13 Q8JIM4	Q8jim4 paralicthy
40	131.5	27.5	101	12 Q8JRS7	Q8jrs7 guinea pig
41	130	27.2	32	4 Q9UBG2	Q9ubg2 homo sapien
42	130	27.2	98	6 Q8HYP7	Q8hy p7 macaca mula
43	128.5	26.9	94	6 Q8HYP9	Q8hy p9 macaca mula
44	127	26.6	95	13 Q8AYB2	Q8ayb2 ictalurus p
45	126.5	26.5	119	11 Q8K477	Q8k477 rattus norv

## ALIGNMENTS

### RESULT 1

Q8HYQ1	PRELIMINARY;	PRT;	91 AA.
ID Q8HYQ1			
AC Q8HYQ1;			
DT 01-MAR-2003 (TRENBLrel. 23, Created)			
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)			
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)			
DE Chemokine CCL5/RANTES.			
OS Macaca mulatta (Rhesus macaque).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC Cercopithecinae; Macaca.			
OX NCBI_TaxID=9544;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;			
RT "Comprehensive cloning and sequencing reveals evolutionary			
RT conservation among all groups of rhesus macaque chemokines.";			
RL Submitted (NOV-2001) to the EMBL/GenBank/DDAJ databases.			
DR EMBL; AF449268; AAN76072.1; "			
SQ SEQUENCE 91 AA; 10019 MW; BCBD59ED0573803B CRC64;			

Query Match 98.1%; Score 469; DB 6; Length 91;  
Best Local Similarity 96.7%; Pred. NO. 1.7e-47;  
Matches 88; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1	MKVSAARLAVILIATLALCAPASAPSYSDTTPCCPAYIARPLPRAHIKEYEYVTSKCSNP 60	
Db 1	MKVSAARLAVILVALCAPASAPSHASDTTPCCPAYIARPLPRAHIKEYEYVTSKCSNP 60	

QY 61	AVVFTVRKNQVCANPEKKWVRVYINSLEMS 91	
Db 61	AVVFTVRKNQVCANPEKKWVRVYINSLEMS 91	

### RESULT 2

Q8MKD0	PRELIMINARY;	PRT;	91 AA.
ID Q8MKD0			
AC Q8MKD0;			

```

01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Small inducible cytokine A5 RANTES.
Equis caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
[1]
SEQUENCE FROM N.A.
Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
"Equus caballus RANTES mRNA.";
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AF506970; AAC34212.1;
InterPro: IPR000827; CC_ChemKine_sml.
InterPro: IPR001811; Chemokine_IL8.
Pfam: PF00048; IL8; 1.
SMART: SM00199; SCY; 1.
PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
SEQUENCE 91 AA; 10159 MW; AEB253E8CD4ED7FD CRC64;

Query Match      84.9%; Score 406; DB 6; Length 91;
Best Local Similarity 83.5%; Pred. No. 4.2e-40;
Matches 76; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

> 1 MKVSAARLAVILIALTALCAPASAPYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60
> 1 MKVFAALAVILATATCTCPASAPYSDTTPCCFAYISRPLPRAHIQVEYFYTSKCSIP 60
> 61 AVVFTRKRVQCANPEKKWREYINSLEMS 91
> 61 AVVFTRKRVQCANPEKKWREYINTLEMS 91

RESULT 3
> Q8HVS0 PRELIMINARY; PRT; 91 AA.
> Q8HVS0;
> 01-MAR-2003 (TrEMBLrel. 23, Created)
> 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
> 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
> RANTES protein.
> Canis familiaris (Dog).
> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
> Mammalia; Eutheria; Carnivora; Canidae; Canis.
> NCBI_TaxID=9615;
> [1]
> SEQUENCE FROM N.A.
> Enomoto A., Kano R., Hasegawa A.;
> "molecular cloning of canine RANTES gene.";
> Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
> EMBL: AB098562; BAC53725.1;
> SEQUENCE 91 AA; 10179 MW; 01D79538CB8148E7 CRC64;

Query Match      77.4%; Score 370; DB 6; Length 91;
Best Local Similarity 75.8%; Pred. No. 7.1e-36;
Matches 69; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

> 1 MKVSAARLAVILIALTALCAPASAPYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60
> 1 MKVSAATAILLATATFPAPASAPYSDTTPCCFAYISGLPPTHVQVEYFYTSKCSMP 60
> 61 AVVFTRKRVQCANPEKKWREYINSLEMS 91
> 61 AVVFTRKRVQCANPEKKWREYINSLEMS 91

RESULT 4
> Q8SQ40 PRELIMINARY; PRT; 92 AA.
> Q8SQ40;
> 01-JUN-2002 (TrEMBLrel. 21, Created)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DR RANTES protein.
GN RANTES.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura T., Kano R., Hasegawa A.;
RT "molecular cloning of feline RANTES gene.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB083479; BAB89940.1;
DR InterPro: IPR000827; CC_ChemKine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
DR SEQUENCE 92 AA; 10167 MW; 2E6F087140BA3CE8 CRC64;

Query Match      75.8%; Score 362.5; DB 6; Length 92;
Best Local Similarity 72.8%; Pred. No. 5.5e-35;
Matches 67; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 1 MKVSAARLAVILIALTALCAPASAPYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60
DB 1 MKVSAARLAVILIALTALCAPASAPYSDTTPCCFAYISGLPPTHVQVEYFYTSKCSMP 60
QY 61 AVVFTRKRVQCANPEKKWREY-INSLEMS 91
DB 61 AVVFTRKRVQCANPEKKWVRDKGINSLEMN 92

RESULT 5
> Q8QG57 PRELIMINARY; PRT; 91 AA.
> Q8QG57;
> 01-JUN-2002 (TrEMBLrel. 21, Created)
> 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
> 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
> Chemokine ah294.
> Gallus gallus (Chicken).
> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
> OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.
> OC NCBI_TaxID=9031;
> [1]
> SEQUENCE FROM N.A.
> MEDLINE=21655115; PubMed=11797102;
> Hughes S., Haynes A., O'Regan M., Bumstead N.;
> "Identification, mapping, and phylogenetic analysis of three novel
> chicken CC chemokines.";
> Immunogenetics 53:674-683(2001).
> EMBL: AV037859; AAK84432.1;
> InterPro: IPR000827; CC_ChemKine_sml.
> InterPro: IPR001811; Chemokine_IL8.
> Pfam: PF00048; IL8; 1.
> SMART: SM00199; SCY; 1.
> PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
> SEQUENCE 91 AA; 10153 MW; 744R64BB229194EF CRC64;

Query Match      59.5%; Score 284.5; DB 13; Length 91;
Best Local Similarity 57.8%; Pred. No. 7.9e-26;
Matches 52; Conservative 15; Mismatches 22; Indels 1; Gaps 1;

QY 1 MKVSAARLAVILIALTALCAPASAPYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60
DB 2 MTAVAVSLSLIVA-ALFPQASSPPGADTTCFNFYSVRKLPQNHVQDYFYTSKCPQA 60
QY 61 AVVFTRKRVQCANPEKKWREYINSLEMN 90
DB 61 AVVFTRKRVQCANPDARWKEYINFLEL 90

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ULT 10
WAG Q9PWA6 PRELIMINARY; PRT; 90 AA.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Chenokine.
SCYA4.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
Hughes S.M., Bumstead N.,
"Mapping of the gene encoding the chicken homologue of the mammalian
chemokine SCYA4.",
Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF146730; AAD48772.1; -.
HSP; P13236; 1HUM.
InterPro: IPR000827; CC_chemokine_sml.
InterPro: IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SEQUENCE 90 AA; 9986 MW; 50AF5679A26751CB CRC64;

Query Match 52.0%; Score 248.5; DB 13; Length 90;
Best Local Similarity 50.0%; Pred. No. 1.3e-21;
Matches 46; Conservative 20; Mismatches 23; Indels 3; Gaps 2;

1 MKVSAARLAVILIATLALCAPASAPYSSD-TTPCCFYAIARPLPRAHIKEYFYTSKCSN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MKVSAARLAVILIATLALCAPASAPYSSD-TTPCCFYAIARPLPRAHIKEYFYTSKCSN 58

60 PAVVFTKRNQVNCANPEKKVREYINSLEMS 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
59 AGVVFTRKGRVNCANPQNDWQDYNNKELN 90

Query Match 48.5%; Score 232; DB 11; Length 92;
Best Local Similarity 47.8%; Pred. No. 1.2e-19;
Matches 44; Conservative 18; Mismatches 28; Indels 2; Gaps 2;

1 MKVSAARLAVILIATLALCAPASAPYSSD-TTPCCFYAIARPLPRAHIKEYFYTSKCSN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MKVPTAVLAVLLCIITLCNQVFSAPYGADTFTCCFSY-GRQIPKFIADYFQTSLSCE 59

60 PAVVFTKRNQVNCANPEKKVREYINSLEMS 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 PGIFLTKRNHVCADPKETWVQBIITDLELN 91

ULT 11
LZLO Q91ZL0 PRELIMINARY; PRT; 92 AA.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein 1 beta.
MIP-1BETA.
Sigmodon hispidus (Hispid cotton rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
Sigmodon.
NCBI_TaxID=42415;
[1]
SEQUENCE FROM N.A.
Blanco J.C., Pietneva L.M., Prince G.A.;
"Sigmodon hispidus cytokines, chemokines and interferons.",
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF421392; AAL16933.1; -.
HSP; Q9Y258; IG2S.
InterPro: IPR000827; CC_chemokine_sml.
InterPro: IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SEQUENCE 92 AA; 10195 MW; A34FDE21E6FA9C2E CRC64;

Query Match 51.8%; Score 247.5; DB 11; Length 92;
Best Local Similarity 46.7%; Pred. No. 1.8e-21;
Matches 43; Conservative 21; Mismatches 27; Indels 1; Gaps 1;

1 MKVSAARLAVILIATLALCAPASAPYSSD-TTPCCFYAIARPLPRAHIKEYFYTSKCSN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MKVPTAVLAVLLCIITLCNQVFSAPYGADTFTCCFSY-GRQIPKFIADYFQTSLSCE 59

60 PAVVFTKRNQVNCANPEKKVREYINSLEMS 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 PGIFLTKRNHVCADPKETWVQBIITDLELN 91

RESULT 12
Q91Z65 PRELIMINARY; PRT; 92 AA.
ID Q91Z65
AC Q91Z65
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Macrophage inflammatory protein-1 alpha.
GN MIP1 ALPHA.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
Blanco J.C., Pietneva L.M., Prince G.A.;
"Sigmodon hispidus cytokines, chemokines and interferons.",
Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AY059407; AAL26704.1; -.
HSP; Q9Y258; IG2S.
InterPro: IPR000827; CC_chemokine_sml.
InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10334 MW; CF9AAB3D94DCAF79 CRC64;

Query Match 48.5%; Score 232; DB 11; Length 92;
Best Local Similarity 47.8%; Pred. No. 1.2e-19;
Matches 44; Conservative 18; Mismatches 28; Indels 2; Gaps 2;

1 MKVSAARLAVILIATLALCAPASAPYSSD-TTPCCFYAIARPLPRAHIKEYFYTSKCSN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MKVPTAVLAVLLCIITLCNQVFSAPYGADTFTCCFSY-GRQIPKFIADYFQTSLSCE 59

60 PAVVFTKRNQVNCANPEKKVREYINSLEMS 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 PGIFLTKRNHVCADPKETWVQBIITDLELN 91

RESULT 13
Q9NHW4 PRELIMINARY; PRT; 92 AA.
ID Q9NHW4
AC Q9NHW4
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Macrophage inflammatory protein-1b2.
GN CCL4L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
Nibbs R.J., Barcellos L.F., Townson J.R.;
"Variation in gene copy number of the human chemokines macrophage
inflammatory protein-1a/CCL3 and macrophage inflammatory protein-
1b/CCL4.",
Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY079147; AAL87008.1; -.
InterPro: IPR000827; CC_chemokine_sml.

```

InterPro: IPR001811; Chemokine\_IL8.

Pfam: PF00048; IL8; 1.

SMART: SM00199; SCV; 1.

PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.

SEQUENCE 92 AA; 10166 MW; 4C8D01E926CDE882 CRC64;

Query Match 48.2%; Score 230.5; DB 4; Length 92;

Best Local Similarity 44.6%; Pred. No. 1.8e-19;

Matches 41; Conservative 22; Mismatches 28; Indels 1; Gaps 1;

1 MKVSAARLAVILATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYEYTSKCSNP 59

1 MKLCVTLSLLVVAFCSLASAPGSDPTACFSYARKLPNRFVVDYETSLCSQ 60

60 PAVFVTRKNQVCANPEKKWVREYINSLE 91

61 PAVFQTKRGKQVCADPSESWSVOEYVVDLELN 92

SULT 14

4745

Q14745 PRELIMINARY; PRT; 80 AA.

01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

LD78 alpha beta precursor (fragment).

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

[1]

SEQUENCE FROM N.A.

TISSUE=Brain;

Ishizuka K., Igata-Yi R., Naruse K., Nakashima H., Ohuchi K.,

Katsuragi S., Kin Y., Ohmoto Y., Nomiya H., Iio M., Miura R.,

Miyakawa T.,

Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

EMBL: D63785; BAA09855.1; -.

HSSP: P13236; IHUM.

InterPro: IPR000827; CC chemokine sm1.

InterPro: IPR001811; Chemokine\_IL8.

Pfam: PF00048; IL8; 1.

SMART: SM00199; SCV; 1.

PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.

Signal.

NON\_TER

<1 1

SIGNAL

16 POTENTIAL.

17 >80

CHAIN

80 LD78 ALPHA BETA.

NON\_TER

80

SEQUENCE

80 AA; 8857 MW; 8B509EB15648E971 CRC64;

Query Match 44.6%; Score 213; DB 4; Length 80;

Best Local Similarity 45.6%; Pred. No. 1.7e-17;

Matches 36; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

8 LAVILATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYEYTSKCSNPVAVFVTR 67

2 LAVLLCTMALCNQFSASLAADTTACCFYSYRKQIPQNFADYFETSSQCKSPVIFLTK 61

68 KNRQVCANPEKKWVREYIN 86

62 RGRQVCADPSEPSEWQVYVS 80

SULT 15

18E0

Q918E0 PRELIMINARY; PRT; 89 AA.

01-OCT-2000 (TrEMBLrel. 15, Created)

01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Chemokine K203 precursor.

GN K203.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20170941; PubMed=10704244;

RA Sick C., Schneider K., Staeheli P., Weining K.C.;

RT "Novel chicken CXK and CC chemokines.";

BL Cytochrome 12:181-186 (2000).

DR EMBL: Y18692; CAB70956.1; -.

DR HSSP: P13236; IHUM.

DR InterPro: IPR001811; Chemokine\_IL8.

DR Pfam: PF00048; IL8; 1.

DR SMART: SM00199; SCV; 1.

KW SIGNAL.

FT SIGNAL

FT CHAIN

FT SEQUENCE

89 AA; 9896 MW; 6FA2EA7A4950CA75 CRC64;

Query Match 44.6%; Score 213; DB 13; Length 89;

Best Local Similarity 42.7%; Pred. No. 1.9e-17;

Matches 38; Conservative 19; Mismatches 30; Indels 2; Gaps 1;

QY 1 MKVSAARLAVILATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYEYTSKCSNP 60

Db 1 MKLSAVLLA--LLIASFCSSRASSAPVGPDPVTCCTTITHKIPRNLQIRHYSTSCSKP 58

QY 61 AVFVTRKNQVCANPEKKWVREYINSLE 89

Db 59 AIIFITKKEREVCANPSPDPVQRYLQSVK 87

Search completed: December 16, 2003, 15:39:37

Job time : 31.3333 secs



Example: Fig 1: 33pp: English.

CC This sequence represents the C-C chemokine RANTES. The invention relates  
CC to amino-terminally truncated C-C chemokines, having chemokine  
CC antagonistic activity. The truncated chemokines are specifically  
CC residues 26 to 91 of the RANTES sequence (this sequence) or residues 29  
CC to 99 of the MCP2 sequence (see AAY05300). The new chemokines are useful  
CC as medicaments, for diagnosis and/or treatment of diseases which require  
CC antagonistic activity of a chemokine e.g. inflammatory diseases, HIV  
CC infection, tumours, and angiogenesis- and haematopoiesis-related  
CC diseases. The invention also relates to the use of CD36/APP IV for

1 treatment of inflammatory, immune and infectious diseases, including  
 2 autoimmune diseases, atherosclerosis, pulmonary diseases and skin  
 3 disorders.

4 Sequence 91 AA;

5 Query Match 100.0%; Score 478; DB 20; Length 91;  
 6 Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
 7 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 1 MKVSAARLAVILIATATCAPASAPYSSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60

9 1 MKVSAARLAVILIATATCAPASAPYSSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60

10 61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

11 61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

12 RESULT 4

13 AY07235

14 AAY07235 standard; protein; 91 AA.

15 AAY07235;

16 06-JUL-1999 (first entry)

17 Wild type RANTES protein.

18 Wild type; C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV;  
 19 regulated on activation normal T-cell expressed and secreted; RANTES;  
 20 truncation; antagonist; medicaments; diagnosis; inflammation; infection;  
 21 tumour; angiogenesis; hematopoiesis; autoimmune disease; atherosclerosis;  
 22 pulmonary disease; skin disorder.

23 Homo sapiens.

24 EP905241-A1.

25 31-MAR-1999.

26 10-MAR-1998; 98EP-0104216.

27 19-DEC-1997; 97EP-0122471.

28 29-SEP-1997; 97EP-0116863.

29 (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

30 Proost P, Struyf S, Van Damme J;

31 WPI; 1999-206774/18.

32 New amino-terminally truncated C-C chemokines have antagonistic  
 33 activity for treatment of immune, inflammatory and infectious  
 34 diseases

35 Disclosure; Fig 1; 36pp; English.

36 This sequence represents the wild type C-C chemokine Regulated on  
 37 Activation Normal T-cell Expressed and Secreted (RANTES). The invention  
 38 relates the generation of amino-terminal truncated C-C chemokines, having  
 39 chemokine antagonistic activity. The new chemokines are useful as  
 40 medicaments, for diagnosis and/or treatment of diseases which require  
 41 antagonistic activity of a chemokine e.g. inflammatory diseases,  
 42 HIV infection, tumours, and angiogenesis- and hematopoiesis-related  
 43 diseases, including auto-immune diseases, atherosclerosis, pulmonary  
 44 diseases and skin disorders.

45 Sequence 91 AA;

46 Query Match 100.0%; Score 478; DB 20; Length 91;

47 Best Local Similarity 100.0%; Pred. No. 3.1e-46;

48 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATATCAPASAPYSSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
 DB 1 MKVSAARLAVILIATATCAPASAPYSSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60

QY 61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

DB 61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

RESULT 5

AA07231

ID AAY07231 standard; protein; 91 AA.

XX AAY07231;

DT 06-JUL-1999 (first entry)

DE Wild type RANTES protein.

XX Wild type; C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV;  
 KW regulated on activation normal T-cell expressed and secreted; RANTES;  
 KW truncation; antagonist; medicaments; diagnosis; inflammation; infection;  
 KW tumour; angiogenesis; hematopoiesis; autoimmune disease; atherosclerosis;  
 KW pulmonary disease; skin disorder.

XX Homo sapiens.

XX EP906954-A1.

XX 07-APR-1999.

XX 29-SEP-1997; 97EP-0116863.

XX 29-SEP-1997; 97EP-0116863.

(ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Proost P, Struyf S, Van Damme J;

XX WPI; 1999-207108/18.

XX New amino-terminally truncated C-C chemokines have antagonistic  
 PT activity for treatment of immune, inflammatory and infectious  
 PT diseases

XX Disclosure; Fig 1; 29pp; English.

XX This sequence represents the wild type C-C chemokine Regulated on  
 CC Activation Normal T-cell Expressed and Secreted (RANTES). The invention  
 CC relates the generation of amino-terminal truncated C-C chemokines, having  
 CC chemokine antagonistic activity. The new chemokines are useful as  
 CC medicaments, for diagnosis and/or treatment of diseases which require  
 CC antagonistic activity of a chemokine e.g. inflammatory diseases,  
 CC HIV infection, tumours, and angiogenesis- and hematopoiesis-related  
 CC diseases, including auto-immune diseases, atherosclerosis, pulmonary  
 CC diseases and skin disorders.

SQ Sequence 91 AA;

Query Match 100.0%; Score 478; DB 20; Length 91;

Best Local Similarity 100.0%; Pred. No. 3.1e-46;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATATCAPASAPYSSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
 DB 1 MKVSAARLAVILIATATCAPASAPYSSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60

QY 61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

DB 61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91



17-JAN-2001 (first entry)  
Human chemokine RANTES SEQ ID NO: 21.  
Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis; monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV; AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia; basophil-mediated disease; myocardial infarction; acute ischaemia; rheumatoid arthritis; contraception.  
Homo sapiens.  
W0200042071-A2.  
20-JUL-2000.  
12-JAN-2000; 2000WO-US00821.  
12-JAN-1999; 99US-0229071.  
17-MAR-1999; 99US-0271192.  
01-DEC-1999; 99US-0452406.  
(NEOR-) NEORX CORP.  
Grainger DJ, Tatalick LM;  
WPI; 2000-499101/44.  
N-PSDB; AAA74884.  
New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and for treating e.g. stroke, vascular diseases, autoimmune diseases and tumour growth -  
Example 1; Page 134; 387pp; English.  
The present invention concerns the identification of a number of chemokines which can be used to produce derivatives, agonists and antagonists which are then useful in disease treatment. The chemokines include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848. These chemokine derivatives can be used to treat diseases such as autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated diseases, endotoxaemia, myocardial infarction, acute ischaemia and rheumatoid arthritis, and can be used to prevent strokes and as contraceptives. The coding sequences for the chemokines can be used in gene therapy for the same diseases, as well as in the production of animal models.  
Sequence 91 AA;  
Query Match 100.0%; Score 478; DB 21; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
QY 1 MKVSAARLAVILIALCAPASAPYSDDTPCCFAYIARPLPRAHKEYFTSGKCSNP 60  
Db 1 MKVSAARLAVILIALCAPASAPYSDDTPCCFAYIARPLPRAHKEYFTSGKCSNP 60  
QY 61 AVFVTRNQRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVFVTRNQRQVCANPEKKWVREYINSLEMS 91  
RESULT 8  
AAU31766  
ID AAU31766 standard; Protein; 445 AA.  
XX AAU31766;  
AC AAU31766;  
XX 18-DEC-2001 (first entry)  
XX

18-JUN-1999 (first entry)  
Amino acid sequence of native RANTES.  
Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral; infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; vWIP; allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPAV; stromal cell derived factor 1; Macrophage Inflammatory protein.  
Homo sapiens.  
W09911655-A1.  
11-MAR-1999.  
31-AUG-1998; 98WO-US18096.  
04-SEP-1997; 97US-0057620.  
(GRYP-) GRYPHON SCI.  
Kent SBH, Siani MA, Simon R, Wilken J;  
WPI; 1999-205128/17.  
New cross-over proteins for treatment of inflammation and infections e.g. AIDS - prepared by ligation of two functional protein modules derived from two different parent molecules  
Example 4; Page 41; 75pp; English.  
The invention relates to a cross-over protein produced by chemical ligation of at least two functional protein modules derived from at least two parent protein molecules. The cross-over proteins can be used in pharmaceutical compositions for therapy of inflammatory and infectious diseases including AIDS, and for indications of hematopoiesis and chemoprotection. They are also useful for treatment of asthma, allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library comprising a collection of cross-over proteins is useful for screening for cross-over proteins that are receptor ligands. The libraries comprise functionally diverse compounds therefore improving the drug discovery process. The proteins and libraries are exemplified by the preparation of cross-over chemokines comprising various combinations of peptide segments derived from RANTES, SDF-1 (stromal cell derived factor 1), vWIP (viral Macrophage inflammatory protein) and other such chemokines. The present sequence represents a native amino acid fragment of RANTES.  
Sequence 91 AA;  
Query Match 100.0%; Score 478; DB 20; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 MKVSAARLAVILIALCAPASAPYSDDTPCCFAYIARPLPRAHKEYFTSGKCSNP 60  
b 1 MKVSAARLAVILIALCAPASAPYSDDTPCCFAYIARPLPRAHKEYFTSGKCSNP 60  
Y 61 AVFVTRNQRQVCANPEKKWVREYINSLEMS 91  
b 61 AVFVTRNQRQVCANPEKKWVREYINSLEMS 91  
RESULT 7  
AB15790  
D AB15790 standard; Protein; 91 AA.  
X AB15790;  
XX

Novel human secreted protein #2257.

Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

Homo sapiens.

WO200179449-A2.

25-OCT-2001.

16-APR-2001; 2001WO-US08656.

18-APR-2000; 2000US-0552929.

26-JAN-2001; 2001US-0770160.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-611725/70.

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -

Claim 20; Page 506; 765pp; English.

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.

Sequence 445 AA;

Query Match 100.0%; Score 478; DB 22; Length 445;  
Best Local Similarity 100.0%; Pred. No. 1.9e-45;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60

1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60

61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

FULT 9  
124003

AAM24003 standard; Protein; 91 AA.

AAM24003;

12-OCT-2001 (first entry)

Human EST encoded protein SEQ ID NO: 1528.

Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition.

OS Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

XX 25-JAN-2000; 2000US-0491404.

XX 17-JUL-2000; 2000US-0617746.

XX 03-AUG-2000; 2000US-0631451.

XX 15-SEP-2000; 2000US-0663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.

XX N-PSDB; AAH98662.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use -

XX Claim 20; Page 1053; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel  
XX proteins from a variety of organisms, including human, dog, cat, horse,  
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)  
XX from the organism of interest. They can be used in diagnostics,  
XX forensics, gene mapping, identification of mutations, to assess  
XX biodiversity and for nutritional purposes. The present sequence is a  
XX protein of the invention.

XX Sequence 91 AA;

Query Match 98.7%; Score 472; DB 22; Length 91;

Best Local Similarity 98.9%; Pred. No. 1.5e-45;

Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60

Db 1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60

QY 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

Db 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

RESULT 10

ABB80929  
ID ABB80929 standard; Protein; 91 AA.

XX ABB80929;

XX 08-OCT-2002 (first entry)

XX Human RANTES protein sequence.

XX Paramyxovirus; infection; RANTES; chemokine; antiviral; CCR1; CCR5;  
KW apoptosis; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..23

FT Protein 24..91 /note= "signal peptide"

FT /note= "specifically claimed mature protein"

WO200255019-A2.

18-JUL-2002.

23-OCT-2001; 2001WO-US45244.

24-OCT-2000; 2000US-243264P.

(UNIW ) UNIV WASHINGTON.

Holtzman MJ;

WPI; 2002-566709/60.

Use of RANTES chemokine or an expression system in treatment and diagnosis of paramyxovirus infection, especially in children -

Claim 5; Page -; 19pp; English.

The invention relates to the treatment of paramyxovirus infection that involves administration of an active ingredient such as RANTES chemokine (I) or an expression system (II). (I) and (II) are used in the treatment and diagnosis of paramyxoviral infection, especially in children. RANTES chemokine has a significant effect on respiratory infections caused by paramyxovirus. RANTES acts downstream of viral entry and signals through specific CCR1 and/or CCR5 chemokine receptors to interrupt the death pathway of macrophages which have been infected by virus. RANTES not only inhibits apoptosis of infected macrophage but also clears the macrophage of infection. The present sequence represents a human RANTES protein. Note: the present sequence is not provided in the specification. It has been obtained from the NCBI database under the accession no. NP\_002976.

Sequence 91 AA;

Query Match 98.7%; Score 472; DB 23; Length 91;  
Best Local Similarity 98.9%; Pred. No. 1.5e-45;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSSDTTCCCFAYIARPLPRAHIKEYFTYSGKCSNP 60

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1 MKVSAARLAVILIATLALCAPASAPSYSSDTTCCCFAYIARPLPRAHIKEYFTYSGKCSNP 60

61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

SULT 11

321079

RAO21079 standard; Protein; 91 AA.

RAO21079;

19-JUL-2002 (first entry)

Wild type RANTES protein.

RANTES; neuroprotective; anti-allergic; anti-inflammatory; anti-HIV; human; chemokine mutant; cationic site; multiple sclerosis; HIV infection; inflammatory disease; demyelinating disease; allergic; wild type.

Homo sapiens.

WO200228419-A2.

11-APR-2002.

03-OCT-2001; 2001WO-EP11428.

04-OCT-2000; 2000EP-0121665.

(ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Proudfoot A, Wells TNC, Kosco-Vilbois M;

XX WPI; 2002-340073/37.

XX A mutant of the human CC chemokine RANTES with two mutations in the

XX cationic site of the 40's loop is used for treatment of multiple

XX sclerosis and/or demyelinating diseases -

XX Examples; Page 36; 46pp; English.

XX The invention relates to a truncated and mutated human RANTES (a CC

XX chemokine mutant), comprising the amino sequence of 91 amino acids as

XX given in the specification. The CC chemokine mutant RANTES, with two

XX mutations in the cationic site is useful for the preparation of a

XX pharmaceutical composition used in treating multiple sclerosis or other

XX demyelinating diseases. The mutant with single mutations at cationic

XX sites is used for the treatment of HIV infection and/or other allergic or

XX inflammatory diseases. This sequence represents the wild-type human

XX RANTES protein of the invention.

XX SQ Sequence 91 AA;

Query Match 98.7%; Score 472; DB 23; Length 91;

Best Local Similarity 98.9%; Pred. No. 1.5e-45;

Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTTCCCFAYIARPLPRAHIKEYFTYSGKCSNP 60

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

1 MKVSAARLAVILIATLALCAPASAPSYSSDTTCCCFAYIARPLPRAHIKEYFTYSGKCSNP 60

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

RESULT 12

RAO21079

ID AAM52443 standard; Protein; 91 AA.

XX AAM52443;

XX 03-JUL-2002 (first entry)

XX HIV\_Nef1 fusion protein #10.

XX Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.

XX Homo sapiens.

XX US6303295-B1.

XX 16-OCT-2001.

XX 12-JUL-1996; 96US-0679493.

XX 14-JUL-1995; 95US-001203P.

XX 01-SEP-1995; 95US-003112P.

XX (UNGE-) UNIV GEORGIA RES FOUND INC.

XX Taylor EW, Nadimpalli RG, Ramanathan CS;

XX WPI; 2002-024734/03.

XX New selenoprotein for use in detecting certain viruses, e.g. human

XX immunodeficiency virus (HIV) or Ebola, cancer and immune system

XX disorders -

XX Disclosure; Columns 73-76; 140pp; English.

XX The present invention relates to selenoproteins encoded in the genome of

XX a virus, where the coding sequence of the selenoprotein is genetically

C engineered for expression in a nucleic acid construct. The invention also  
 C discloses a method for identifying selenoprotein coding sequences, for  
 C detecting certain viruses (e.g. HIV or Ebola), cancer and immune system  
 C disorders. The present sequence was used to illustrate the invention.

X Sequence 91 AA;

Query Match 98.7%; Score 472; DB 23; Length 91;

Best Local Similarity 98.9%; Pred. No. 1.5e-45;

Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60

b 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60

Y 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

b 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 13

AAO21086

D AAO21086 standard; Protein; 91 AA.

X AAO21086;

X T 19-JUL-2002 (first entry)

X Protein of R44A-RANTES mutant.

X RANTES; neuroprotective; anti-allergic; anti-inflammatory; anti-HIV; human;

X Chemokine mutant; cationic site; multiple sclerosis; HIV infection;

X inflammatory disease; demyelinating disease; allergic; mutein.

X Homo sapiens.

X Synthetic.

X WO200228419-A2.

X 11-APR-2002.

X 03-OCT-2001; 2001WO-EPI1428.

X 04-OCT-2000; 2000EP-0121665.

X (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

X Proudfoot A, Wells TNC, Kosco-Vilbois M;

X WPI; 2002-340073/37.

X A mutant of the human CC chemokine RANTES with two mutations in the

X cationic site of the 40's loop is used for treatment of multiple

X sclerosis and/or demyelinating diseases -

X Examples; Page 39; 46pp; English.

X The invention relates to a truncated and mutated human RANTES (a CC

X chemokine mutant), comprising the amino sequence of 91 amino acids as

X given in the specification. The CC chemokine mutant RANTES, with two

X mutations in the cationic site is useful for the preparation of a

X pharmaceutical composition used in treating multiple sclerosis or other

X demyelinating diseases. The mutant with single mutations at cationic

X sites is used for the treatment of HIV infection and/or other allergic or

X inflammatory diseases. This sequence represents a mutant human RANTES

X protein of the invention.

X Sequence 91 AA;

X Query Match 97.5%; Score 466; DB 23; Length 91;

X Best Local Similarity 97.8%; Pred. No. 6.9e-45;

X Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

X Y 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60

b 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60

Y 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

b 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 14

AAO21087

ID AAO21087 standard; Protein; 91 AA.

X AAO21087;

X 19-JUL-2002 (first entry)

X Protein of K68A-RANTES mutant.

X RANTES; neuroprotective; anti-allergic; anti-inflammatory; anti-HIV; human;

X Chemokine mutant; cationic site; multiple sclerosis; HIV infection;

X inflammatory disease; demyelinating disease; allergic; mutein.

X Homo sapiens.

X Synthetic.

X WO200228419-A2.

X 11-APR-2002.

X 03-OCT-2001; 2001WO-EPI1428.

X 04-OCT-2000; 2000EP-0121665.

X (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

X Proudfoot A, Wells TNC, Kosco-Vilbois M;

X WPI; 2002-340073/37.

Qy 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60

Db 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60

Qy 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

Db 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 14

AAO21087

ID AAO21087 standard; Protein; 91 AA.

X AAO21087;

X 19-JUL-2002 (first entry)

X Protein of K68A-RANTES mutant.

X RANTES; neuroprotective; anti-allergic; anti-inflammatory; anti-HIV; human;

X Chemokine mutant; cationic site; multiple sclerosis; HIV infection;

X inflammatory disease; demyelinating disease; allergic; mutein.

X Homo sapiens.

X Synthetic.

X Key Location/Qualifiers

X Misc-difference 68 /note= "Wild-type Lys substituted by Ala"

X WO200228419-A2.

X 11-APR-2002.

X 03-OCT-2001; 2001WO-EPI1428.

X 04-OCT-2000; 2000EP-0121665.

X (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

X Proudfoot A, Wells TNC, Kosco-Vilbois M;

X WPI; 2002-340073/37.

X A mutant of the human CC chemokine RANTES with two mutations in the

X cationic site of the 40's loop is used for treatment of multiple

X sclerosis and/or demyelinating diseases -

X Examples; Page 39; 46pp; English.

X The invention relates to a truncated and mutated human RANTES (a CC

X chemokine mutant), comprising the amino sequence of 91 amino acids as

X given in the specification. The CC chemokine mutant RANTES, with two

X mutations in the cationic site is useful for the preparation of a

X pharmaceutical composition used in treating multiple sclerosis or other

X demyelinating diseases. The mutant with single mutations at cationic

X sites is used for the treatment of HIV infection and/or other allergic or

X inflammatory diseases. This sequence represents a mutant human RANTES

X protein of the invention.

X Sequence 91 AA;

X Query Match 97.5%; Score 466; DB 23; Length 91;

X Best Local Similarity 97.8%; Pred. No. 6.9e-45;

X Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

X Y 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60

Db 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60

Qy 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

Db 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91



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6	478	100.0	91	11	U
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8	478	100.0	91	14	U
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10	478	100.0	91	15	U
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12	374	78.2	68	9	US
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14	374	78.2	68	10	U
14	374	78.2	68	10	U

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Mult No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	478	100.0	91	8	US-08-927-939-21		Sequence 21, Appl
2	478	100.0	91	9	US-09-144-838-9		Sequence 9, Appl
3	478	100.0	91	9	US-09-834-795A-29		Sequence 29, Appl
4	478	100.0	91	11	US-09-634-794A-29		Sequence 29, Appl
5	478	100.0	91	11	US-09-920-137A-8		Sequence 8, Appl
6	478	100.0	91	11	US-09-537-658-1		Sequence 1, Appl
7	478	100.0	91	12	US-10-137-655-8		Sequence 8, Appl
8	478	100.0	91	14	US-10-158-366-5		Sequence 5, Appl
9	478	100.0	91	14	US-10-057-275-8		Sequence 8, Appl
10	478	100.0	91	15	US-10-293-705-12		Sequence 12, Appl
11	374	78.2	68	9	US-09-144-838-10		Sequence 10, Appl
12	374	78.2	68	9	US-09-144-838-42		Sequence 42, Appl
13	374	78.2	68	9	US-09-195-457-11		Sequence 11, Appl
14	374	78.2	68	10	US-09-792-793A-29		Sequence 29, Appl
15	374	78.2	68	12	US-10-375-209A-29		Sequence 29, Appl

16	363.5	76.0	69	9	US-09-144-838-46	Sequence 46, Appl
17	363	75.9	66	11	US-09-537-858-2	Sequence 2, Appl
18	332	69.5	60	10	US-09-889-938-5	Sequence 5, Appl
19	325	68.0	67	9	US-09-144-838-38	Sequence 38, Appl
20	318	66.5	67	9	US-09-144-838-41	Sequence 41, Appl
21	317	66.3	68	9	US-09-144-838-40	Sequence 40, Appl
22	316	66.1	68	9	US-09-144-838-34	Sequence 34, Appl
23	307.5	64.3	68	9	US-09-144-838-45	Sequence 45, Appl
24	306.5	64.1	69	9	US-09-144-838-44	Sequence 44, Appl
25	269	56.3	66	9	US-09-144-838-37	Sequence 37, Appl
26	268	56.1	67	9	US-09-144-838-36	Sequence 36, Appl
27	261	54.6	67	9	US-09-144-838-39	Sequence 39, Appl
28	260	54.4	67	9	US-09-144-838-33	Sequence 33, Appl
29	259	54.2	68	9	US-09-144-838-32	Sequence 32, Appl
30	252.5	52.8	93	8	US-08-937-939-49	Sequence 49, Appl
31	252.5	52.8	93	9	US-09-151-450-2	Sequence 2, Appl
32	252.5	52.8	93	9	US-09-834-794A-32	Sequence 32, Appl
33	252.5	52.8	93	11	US-09-834-794A-32	Sequence 32, Appl
34	252.5	52.8	93	12	US-10-260-270-3	Sequence 3, Appl
35	252.5	52.8	93	12	US-10-223-081-330	Sequence 330, App
36	252.5	52.8	93	12	US-10-223-082-330	Sequence 330, App
37	252.5	52.8	93	12	US-10-247-671-119	Sequence 179, App
38	252.5	52.8	93	14	US-10-141-965-6	Sequence 6, Appl
39	252.5	52.8	93	15	US-10-223-085-330	Sequence 330, App
40	252.5	52.8	93	15	US-10-223-084-330	Sequence 330, App
41	252.5	52.8	93	15	US-10-223-088-330	Sequence 330, App
42	252.5	52.8	93	15	US-10-223-090-330	Sequence 330, App
43	252.5	52.8	93	15	US-10-223-087-330	Sequence 330, App
44	252.5	52.8	93	15	US-10-223-089-330	Sequence 330, App
45	252.5	52.8	93	15	US-10-223-083-330	Sequence 330, App

## ALIGNMENTS

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RESULT 1
US-08-927-939-21
; Sequence 21, Application US/08927939
; Publication NO. US2001006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalack, Lauren Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-21

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	Best Local Similarity	100.0%;	Pred. No. 6.4e-47;		
	Matches 91;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	61 AVVFVTRKNRQVCANPEKKWVREYINSLMS	91			
DB	61 AVVFVTRKNRQVCANPEKKWVREYINSLMS	91			

RESULT 2  
US-03-144-838-9  
; Sequence 9, Application US/09144838A  
; Patent No. US20020051996A1  
; GENERAL INFORMATION:

APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
FILE REFERENCE: GREN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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Query Match 100.0%; Score 478; DB 9; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
SULT 3  
-09-834-795A-29  
Sequence 29, Application US/09834795A  
Patent No. US20020076710A1  
GENERAL INFORMATION:  
APPLICANT: Lawrence, Papsidero  
APPLICANT: Lvn, Dyster  
APPLICANT: Jana, Frustaci  
TITLE OF INVENTION: Detection and Treatment of Breast Cancer  
FILE REFERENCE: 3380/11127-US3  
CURRENT APPLICATION NUMBER: US/09/834,795A  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 09/146,580  
PRIOR FILING DATE: 1998-09-03  
PRIOR APPLICATION NUMBER: 60/071,899  
PRIOR FILING DATE: 1998-01-20  
PRIOR APPLICATION NUMBER: 60/092,155  
PRIOR FILING DATE: 1998-07-09  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 29  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
-09-834-795A-29  
Query Match 100.0%; Score 478; DB 9; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
RESULT 4

US-09-834-794A-29  
Sequence 29, Application US/09834794A  
Patent No. US20030026777A1  
GENERAL INFORMATION:  
APPLICANT: Lawrence, Papsidero  
APPLICANT: Lvn, Dyster  
APPLICANT: Jana, Frustaci  
TITLE OF INVENTION: Detection and Treatment of Breast Cancer  
FILE REFERENCE: 3380/11127-US4  
CURRENT APPLICATION NUMBER: US/09/834,794A  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 09/146,580  
PRIOR FILING DATE: 1998-09-03  
PRIOR APPLICATION NUMBER: 60/071,899  
PRIOR FILING DATE: 1998-01-20  
PRIOR APPLICATION NUMBER: 60/092,155  
PRIOR FILING DATE: 1998-07-09  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 29  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-834-794A-29  
Query Match 100.0%; Score 478; DB 11; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
DB 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
QY 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
DB 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
RESULT 5  
US-09-920-137A-8  
Sequence 8, Application US/09920137A  
Patent No. US20030049725A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/920,137A  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE: GerBank  
LIBRARY: RANTES  
CLONE: RANTES  
-09-920-137A-8

Query Match 100.0%; Score 478; DB 11; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
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61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
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SULT 6  
-09-537-858-1  
Sequence 1, Application US/09537858  
Publication No. US20030119148A1  
GENERAL INFORMATION:  
APPLICANT: PROOST, PAUL  
APPLICANT: VAN DAMME, JO  
TITLE OF INVENTION: AMINO-TERMINALLY TRUNCATED RANTES AS CHEMOKINE  
FILE REFERENCE: 2024/49674  
CURRENT APPLICATION NUMBER: US/09/537,858  
CURRENT FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
-09-537-858-1

Query Match 100.0%; Score 478; DB 11; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
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1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
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61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
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SULT 7  
-10-137-655-8  
Sequence 8, Application US/10137655  
Publication No. US20030138917A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto

STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/137,655  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PP-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: RANTES  
US-10-137-655-8

Query Match 100.0%; Score 478; DB 12; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
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QY 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
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DB 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
|||||

RESULT 8  
US-10-158-366-5  
Sequence 5, Application US/10158366  
Publication No. US20020142398A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
Wilde, Craig C.  
Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/158,366  
FILING DATE: 29-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,123B  
FILING DATE: 06-JUN-1995



APPLICATION NUMBER: US 08/375,346  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
-10-158-366-5

Query Match 100.0%; Score 478; DB 14; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

SULT 9  
-10-057-275-8  
Sequence 8, Application US/10057275  
Publication No. US20020155545A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
Bandman, Olga  
Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/057,275  
FILING DATE: 25-Jan-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,740A  
FILING DATE: February 17, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: RANTES  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-057-275-8  
Query Match 100.0%; Score 478; DB 14; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

RESULT 10  
US-10-293-705-12  
Sequence 12, Application US/10293705  
Publication No. US20030083468A1  
GENERAL INFORMATION:  
APPLICANT: Wilde, Craig G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: DNA ENCODING LIVER EXPRESSED CHEMOKINE  
FILE REFERENCE: PF-0024-3 CON  
CURRENT APPLICATION NUMBER: US/10/293,705  
CURRENT FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: 09/208,803  
PRIOR FILING DATE: 1998-12-09  
PRIOR APPLICATION NUMBER: 08/798,143  
PRIOR FILING DATE: 1997-02-10  
PRIOR APPLICATION NUMBER: 08/347,492  
PRIOR FILING DATE: 1994-11-29  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PERL Program  
SEQ ID NO 12  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: GenBank ID No. US20030083468A1 g134510  
US-10-293-705-12

Query Match 100.0%; Score 478; DB 15; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
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1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKRVQVCANPEKKWVREYINSLEMS 91

RESULT 11  
US-09-144-838-10  
Sequence 10, Application US/09144838A  
Patent No. US20020051996A1  
GENERAL INFORMATION:  
APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation

FILE REFERENCE: GRFN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
-09-144-838-10

Query Match 78.2%; Score 374; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNQVCANPEKKWVRE 60  
84 YINSLEMS 91  
61 YINSLEMS 68

SULT 12  
-09-144-838-42  
Sequence 42, Application US/09144838A  
Patent No. US20020051996A1  
GENERAL INFORMATION:  
APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
FILE REFERENCE: GRFN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
-09-144-838-42

Query Match 78.2%; Score 374; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
24 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNQVCANPEKKWVRE 83  
1 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNQVCANPEKKWVRE 60  
84 YINSLEMS 91  
61 YINSLEMS 68

SULT 13  
-09-195-457-11  
Sequence 11, Application US/09195457  
Patent No. US20020081623A1  
GENERAL INFORMATION:  
APPLICANT: WILLIAMS, TIMOTHY J.  
APPLICANT: JOSE, PETER J.

APPLICANT: GRIFFITHS-JOHNSON, DAVID A.  
APPLICANT: HSUAN, JOHN J.  
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE  
FILE REFERENCE: 550-33  
CURRENT APPLICATION NUMBER: US/09/195,457  
CURRENT FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 08/470,323  
PRIOR FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: PCT/GB94/02006  
PRIOR FILING DATE: 1994-09-14  
PRIOR APPLICATION NUMBER: GB 9318984.3  
PRIOR FILING DATE: 1993-09-14  
PRIOR APPLICATION NUMBER: GB 94086902.2  
PRIOR FILING DATE: 1994-04-29  
NUMBER OF SEQ ID NOS: 11  
SEQ ID NO 11  
LENGTH: 68  
TYPE: PRT  
ORGANISM: human  
US-09-195-457-11

Query Match 78.2%; Score 374; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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84 YINSLEMS 91  
61 YINSLEMS 68

RESULT 14  
US-09-792-793A-29  
Sequence 29, Application US/09792793A  
Patent No. US20020186370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE A  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 68  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
OTHER INFORMATION: Human Chemokine Polypeptide: RANTES  
US-09-792-793A-29

Query Match 78.2%; Score 374; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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84 YINSLEMS 91  
61 YINSLEMS 68

RESULT 15  
US-10-375-209A-29  
Sequence 29, Application US/10375209A  
Publication No. US20030215421A1

GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601E  
CURRENT APPLICATION NUMBER: US/10/375,209A  
CURRENT FILING DATE: 2003-02-24  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 68  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
OTHER INFORMATION: Human Chemokine Polypeptide: RANTES  
-10-375-209A-29

Query Match 78.2%; Score 374; DB 12; Length 68;  
Best Local Similarity 100.0%; Pred. NO. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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84 YINSLEMS 91  
|||||  
61 YINSLEMS 68

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db time : 25.3661 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

protein - protein search, using sw model

on: December 16, 2003, 15:37:55 ; Search time 165.59 Seconds  
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500.045 Million cell updates/sec

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Query	Match	Length	ID	Description
1	478	100.0	91	1 PCT-US94-08207A-36

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Sequence 36, Appl
Sequence 36, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 4, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 9, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 22750, A
Sequence 29, Appl
Sequence 29, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 4, Appl
Sequence 12, Appl
Sequence 8708, Ap
Sequence 8708, Ap
Sequence 21, Appl
Sequence 21, Appl
Sequence 16, Appl
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Sequence 21, Appl
Sequence 21, Appl
Sequence 115540,
Sequence 16, Appl
Sequence 1528, Ap
Sequence 1232, Ap
Sequence 9334, Ap
Sequence 289, App
Sequence 13789, A
Sequence 13789, A
Sequence 7331, Ap
Sequence 7331, Ap

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#### ALIGNMENTS

RESULT 1  
PCT-US94-08207A-36  
Sequence 36, Application PC/TUS9408207A  
GENERAL INFORMATION:

APPLICANT: The Upjohn Company  
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND  
TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:

ADDRESSEE: The Upjohn Company, Intellectual Property Law  
STREET: 301 Henrietta  
CITY: Kalamazoo  
STATE: MI  
COUNTRY: USA  
ZIP: 49001

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08207A  
FILING DATE:

## CLASSIFICATION:

## ATTORNEY/AGENT INFORMATION:

NAME: Jameson, William G.

REGISTRATION NUMBER: 27,199

REFERENCE/DOCKET NUMBER: 4731.1 CP

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 616/385-7561

TELEFAX: 616/385-6897

TELEX: 224401

INFORMATION FOR SEQ ID NO: 36:

## SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

T-US94-08207A-36

Query Match 100.0%; Score 478; DB 1; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
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 1 MKVSAARLAVILIATLALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
 |||||

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

## SULT 2

T-US94-08207-36

Sequence 36, Application PC/TUS9408207

## GENERAL INFORMATION:

APPLICANT: Hoogewerf, Arlene J.

TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND

TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Upjohn Company, Intellectual Property Law

STREET: 301 Henrietta

CITY: Kalamazoo

STATE: MI

COUNTRY: USA

ZIP: 49001

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/08207

FILING DATE:

## CLASSIFICATION:

## ATTORNEY/AGENT INFORMATION:

NAME: Jameson, William G.

REGISTRATION NUMBER: 27,199

REFERENCE/DOCKET NUMBER: 4731.1 CP

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 616/385-7561

TELEFAX: 616/385-6897

TELEX: 224401

INFORMATION FOR SEQ ID NO: 36:

## SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

T-US94-08207-36

Query Match 100.0%; Score 478; DB 1; Length 91;

Best Local Similarity 100.0%; Pred. No. 2.9e-46;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
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 DB 1 MKVSAARLAVILIATLALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
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QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

DB 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

## RESULT 3

US-08-136-117-36

Sequence 36, Application US/08136117

## GENERAL INFORMATION:

APPLICANT: Hoogewerf, Arlene J.

TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND

TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Upjohn Company, Intellectual Property Law

STREET: 301 Henrietta

CITY: Kalamazoo

STATE: MI

COUNTRY: USA

ZIP: 49001

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/136,117

FILING DATE:

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Jameson, William G.

REGISTRATION NUMBER: 27,199

REFERENCE/DOCKET NUMBER: 4731.1 CP

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 616/385-7561

TELEFAX: 616/385-6897

TELEX: 224401

INFORMATION FOR SEQ ID NO: 36:

## SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-136-117-36

Query Match 100.0%; Score 478; DB 5; Length 91;

Best Local Similarity 100.0%; Pred. No. 2.9e-46;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
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 DB 1 MKVSAARLAVILIATLALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
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QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

DB 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

## RESULT 4

US-08-390-740B-8

Sequence 8, Application US/08390740B

## GENERAL INFORMATION:

APPLICANT: Coleman, Roger

APPLICANT: Bandman, Olga  
 APPLICANT: Wilde, Craig G.  
 TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/390,740B  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Luther, Barbara J.  
 REGISTRATION NUMBER: 33,954  
 REFERENCE/DOCKET NUMBER: PF-0027 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: RANTES

-08-467-123-8

Query Match 100.0%; Score 478; DB 7; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
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SULT 5

-08-467-123-5  
 Sequence 5, Application US/08467123

GENERAL INFORMATION:  
 APPLICANT: Coleman, Roger  
 APPLICANT: Wilde, Craig G.  
 APPLICANT: Seilhamer, Jeffrey J.  
 TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
 TITLE OF INVENTION: ITS PRODUCTION AND USES  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 STREET: 3330 HILLVIEW AVENUE  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,123  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/375,346  
 FILING DATE: 19-JAN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LUTHER, BARBARA J.  
 REGISTRATION NUMBER: 33,954  
 REFERENCE/DOCKET NUMBER: PF-0026 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 855-0555  
 TELEFAX: (415) 855-0572  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 91 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US-08-467-123-5

Query Match 100.0%; Score 478; DB 8; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
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 DB 1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
 |||||  
 QY 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
 |||||  
 DB 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
 |||||

RESULT 6

US-08-927-939-21  
 Sequence 21, Application US/08927939

GENERAL INFORMATION:  
 APPLICANT: Grainger, David J.  
 APPLICANT: Tatalick, Lauen Marie  
 TITLE OF INVENTION: Compounds and methods to inhibit or  
 TITLE OF INVENTION: augment an inflammatory response.  
 FILE REFERENCE: 295.022US1  
 CURRENT APPLICATION NUMBER: US/08/927,939  
 CURRENT FILING DATE: 1997-09-11  
 NUMBER OF SEQ ID NOS: 83  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 21  
 LENGTH: 91  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-08-927-939-21

Query Match 100.0%; Score 478; DB 13; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
 |||||  
 DB 1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
 |||||  
 QY 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
 |||||  
 DB 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
 |||||

## SULT 7

-08-927-939A-21  
Sequence 21, Application US/08927939A  
GENERAL INFORMATION:  
APPLICANT: Grainger, David J.  
TITLE OF INVENTION: Compounds and methods to inhibit or  
FILE REFERENCE: 1543.001US1  
CURRENT FILING DATE: 1997-11-09  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 21  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
-08-927-939A-21

Query Match 100.0%; Score 478; DB 13; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
61 AVFVTRKQRCVNCANPEKKVREYINSLEMS 91  
61 AVFVTRKQRCVNCANPEKKVREYINSLEMS 91

## SULT 8

-09-023-092-4  
Sequence 4, Application US/09023092  
GENERAL INFORMATION:  
APPLICANT: Hedrick, Joseph A.  
APPLICANT: Wang, Luquan  
APPLICANT: Zlotnik, Albert  
APPLICANT: Murgolo, Nicholas J.  
TITLE OF INVENTION: Mammalian Chemokines; Related Reagents  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,092  
FILING DATE: 13-FEB-1998  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0780  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

## US-09-023-092-4

Query Match 100.0%; Score 478; DB 14; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
61 AVFVTRKQRCVNCANPEKKVREYINSLEMS 91  
61 AVFVTRKQRCVNCANPEKKVREYINSLEMS 91

## RESULT 9

US-09-113-705-8  
Sequence 8, Application US/09113705  
GENERAL INFORMATION:  
APPLICANT: BANDMAN, OLGA  
APPLICANT: COLEMAN, ROGER  
APPLICANT: STUART, SUSAN G.  
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCITE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/113,705  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,144  
FILING DATE: 13-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF-0031 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

## US-09-113-705-8

Query Match 100.0%; Score 478; DB 15; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
61 AVFVTRKQRCVNCANPEKKVREYINSLEMS 91  
61 AVFVTRKQRCVNCANPEKKVREYINSLEMS 91

## RESULT 10

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-09-113-705-5
Sequence 5, Application US/09113705A
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Stuart, Susan G.
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
FILE REFERENCE: EP-0031-1 DIV
CURRENT APPLICATION NUMBER: US/09/113,705A
CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Rantes
-09-113-705-5

Query Match      100.0%; Score 478; DB 15; Length 91;
Best Local Similarity 100.0%; Pred.No.2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPSYSDTTPCCFAVIARPLPRAHIKEYFTSGKCSNP 60
|||||
1 MKVSAARLAVILIATALCAPASAPSYSDTTPCCFAVIARPLPRAHIKEYFTSGKCSNP 60
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61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91
|||||

SULT 11
-09-144-838-9
Sequence 9, Application US/09144838A
GENERAL INFORMATION:
APPLICANT: Siani, Michael A.
APPLICANT: Wilken, Jill
APPLICANT: Simon, Reyna
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
FILE REFERENCE: GRFN-020/01US
CURRENT APPLICATION NUMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 91
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
-09-144-838-9

Query Match      100.0%; Score 478; DB 15; Length 91;
Best Local Similarity 100.0%; Pred.No.2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MKVSAARLAVILIATALCAPASAPSYSDTTPCCFAVIARPLPRAHIKEYFTSGKCSNP 60
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61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91
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SULT 12
-09-150-813-21
Sequence 21, Application US/09150813

```



us-09-920-137a-8.rapm

Dec 16 15:54:10 2003

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,620  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: US 08/467,123  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ballings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0026-1 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-555-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-387-620-5

Query Match 100.0%; Score 478; DB 17; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
DB 1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
DB 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

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Job time: 165.59 secs

TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
FORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 134510  
-208-803-12

ry Match 100.0%; Score 478; DB 16; Length 91;  
t Local Similarity 100.0%; Pred. No. 2.9e-46;  
ches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

Sequence 5, Application US/09360290  
GENERAL INFORMATION:  
PPLICANT: Bandman, Olga  
PPLICANT: Coleman, Roger  
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS  
TITLE REFERENCE: PF-0031-2 Div  
CURRENT APPLICATION NUMBER: US/09/360,290  
CURRENT FILING DATE: 1999-07-22  
EARLIER APPLICATION NUMBER: 08/421,144  
EARLIER FILING DATE: 1995-04-13  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq Version 3.0  
SEQ ID NO 5  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Rantes  
09-360-290-5

Query Match 100.0%; Score 478; DB 17; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

SULT 15  
-09-387-620-5  
Sequence 5, Application US/09387620  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig C.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
TITLE OF INVENTION: ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9

GenCore version 5.1.6  
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protein - protein search, using sw model

on: December 16, 2003, 15:38:25 ; Search time 13.4262 Seconds  
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Gapop 10.0 , Gapext 0.5

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Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata2/paa/US06\_NEW\_COMB.pcp.\*  
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7: /cgn2\_6/prodata2/paa/US60\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

seq No.	Score	Query Match	Length	ID	Description
1	472	98.7	91	6	US-10-398-457-1
2	472	98.7	91	7	US-60-487-610-2474
3	472	98.7	91	7	US-60-485-450-1561
4	466	97.5	91	6	US-10-398-457-8
5	466	97.5	91	6	US-10-398-457-9
6	466	97.5	91	6	US-10-398-457-10
7	466	97.5	91	6	US-10-398-457-11
8	466	97.5	91	6	US-10-398-457-12
9	466	97.5	91	6	US-10-398-457-13
10	454	95.0	91	6	US-10-398-457-3
11	454	95.0	91	6	US-10-398-457-6
12	443.5	92.8	92	6	US-10-398-457-7
13	374	78.2	68	1	PCT-US03-28745-4
14	374	78.2	68	6	US-10-622-134-11
15	374	78.2	68	6	US-10-332-038A-2
16	345	72.2	66	6	US-10-398-457-2
17	248	51.9	92	1	PCT-US03-21703-42
18	247	51.7	92	7	US-60-487-610-1678
19	247	51.7	92	7	US-60-485-450-1058
20	242.5	50.7	92	7	US-60-487-610-1666
21	242.5	50.7	92	7	US-60-487-610-1677
22	242.5	50.7	92	7	US-60-485-450-1051
23	242.5	50.7	92	7	US-60-485-450-1057
24	199.5	41.7	69	1	PCT-US03-28745-3
25	199.5	41.7	69	6	US-10-622-134-9
26	199.5	41.7	69	6	US-10-332-038A-9

27	199.5	41.7	70	6	US-10-332-038A-8	Sequence 8, Appli
28	199.5	41.7	70	6	US-10-398-457-31	Sequence 31, Appli
29	198.5	41.5	68	6	US-10-622-134-10	Sequence 10, Appli
30	190.5	39.9	69	6	US-10-398-457-5	Sequence 5, Appli
31	186	38.9	33	1	PCT-US03-28745-885	Sequence 885, App
32	186	38.9	33	1	PCT-US03-28745-930	Sequence 930, App
33	186	38.9	93	6	US-10-474-794-277	Sequence 277, App
34	186	38.9	93	6	US-10-474-794-279	Sequence 279, App
35	186	38.9	93	6	US-10-474-794-281	Sequence 281, App
36	186	38.9	93	7	US-60-487-610-2476	Sequence 2476, Ap
37	184.5	38.5	70	6	US-10-398-457-4	Sequence 4, Appli
38	182.5	38.2	89	7	US-60-487-610-2330	Sequence 2330, Ap
39	177.5	37.1	100	1	PCT-US03-28227-4411	Sequence 4411, Ap
40	174.5	36.5	94	7	US-60-487-610-2730	Sequence 2730, Ap
41	172	36.0	74	6	US-10-332-038A-15	Sequence 15, Appli
42	172	36.0	74	6	US-10-398-457-35	Sequence 35, Appli
43	167	34.9	99	1	PCT-US03-21703-41	Sequence 41, Appli
44	167	34.9	99	6	US-10-646-770-18	Sequence 18, Appli
45	165.5	34.6	120	7	US-60-487-610-2473	Sequence 2473, Ap

ALIGNMENTS

RESULT 1

US-10-398-457-1  
; Sequence 1, Application US/10398457  
; GENERAL INFORMATION:  
; APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
; TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
; FILE REFERENCE: WO465  
; CURRENT APPLICATION NUMBER: US/10/398,457  
; CURRENT FILING DATE: 2003-11-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(23)  
US-10-398-457-1

Query Match 98.7%; Score 472; DB 6; Length 91;  
Best Local Similarity 98.9%; Pred. No. 6.4e-46;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKVSAARLAVILIATLALCAPASAPSYSDTTCCFPAYIARPLPRAHIKEYFYTSKCSNP	60
Db	1	MKVSAARLAVILIATLALCAPASAPSYSDTTCCFPAYIARPLPRAHIKEYFYTSKCSNP	60
Qy	61	AVFVTRKNROVCANPEKKVREYINSLEMS	91
Db	61	AVFVTRKNROVCANPEKKVREYINSLEMS	91

RESULT 2

US-60-487-610-2474  
; Sequence 2474, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; FILE REFERENCE: METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2474  
; LENGTH: 91

TYPE: PRT  
ORGANISM: Homo sapiens  
-60-487-610-2474

Query Match 98.7%; Score 472; DB 7; Length 91;  
Best Local Similarity 98.9%; Pred. No. 6.4e-46; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
61 AVFVTRKQVQCANPEKKWREYINSLEMS 91  
61 AVFVTRKQVQCANPEKKWREYINSLEMS 91

SULT 3  
-60-485-450-1561  
Sequence 1561, Application US/60485450  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: CL001470  
CURRENT APPLICATION NUMBER: US/60/485,450  
CURRENT FILING DATE: 2003-07-09  
NUMBER OF SEQ ID NOS: 47859  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 1561  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
-60-485-450-1561

Query Match 98.7%; Score 472; DB 7; Length 91;  
Best Local Similarity 98.9%; Pred. No. 6.4e-46; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
61 AVFVTRKQVQCANPEKKWREYINSLEMS 91  
61 AVFVTRKQVQCANPEKKWREYINSLEMS 91

RESULT 4  
-10-398-457-8  
Sequence 8, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
-10-398-457-8  
Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45; Indels 0; Gaps 0;

Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
DB 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
QY 61 AVFVTRKQVQCANPEKKWREYINSLEMS 91  
DB 61 AVFVTRKQVQCANPEKKWREYINSLEMS 91

RESULT 5  
US-10-398-457-9  
Sequence 9, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 9  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
US-10-398-457-9

Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45; Indels 0; Gaps 0;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
DB 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
QY 61 AVFVTRKQVQCANPEKKWREYINSLEMS 91  
DB 61 AVFVTRKQVQCANPEKKWREYINSLEMS 91

RESULT 6  
US-10-398-457-10  
Sequence 10, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
US-10-398-457-10

Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45; Indels 0; Gaps 0;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
DB 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60  
QY 61 AVFVTRKQVQCANPEKKWREYINSLEMS 91



us-09-920-137a-8.rapn

Dec 16 15:54:10 2003

ARE: PatentIn version 3.0

NO 6

TH: 91

IS: PRT

USM: Escherichia coli

URE: SIGNAL

3/KEY: (1) (23)

ATION: (1) (23)

98-457-6

Match 95.0%; Score 454; DB 6; Length 91;

Local Similarity 95.6%; Pred. No. 6.7e-44; Indels 0; Gaps 0;

es 87; Conservative 0; Mismatches 4;

1 MKVSAARLAVILIATLALCAPASASPSSDTPCCFAYIARPLPRAHKEYFTYSGKCSNP 60

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ULT 13

-US03-28745-4

sequence 4, Application PC/TUS0328745

GENERAL INFORMATION: CHEMOKINE THERAPEUTICS CORP.

APPLICANT: CHEMOKINE THERAPEUTICS CORP.

TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES

FILE REFERENCE: 59296.00003

CURRENT APPLICATION NUMBER: PCT/US03/28745

CURRENT FILING DATE: 2003-09-11

NUMBER OF SEQ ID NOS: 1640

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4

LENGTH: 68

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence: Synthetic peptide

OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

JT-US03-28745-4

Query Match

78.2%; Score 374; DB 1; Length 68;

Best Local Similarity 100.0%; Pred. No. 4.5e-35; Indels 0; Gaps 0;

Mismatches 0; Conservative 68;

24 SPYSSDTPCCFAYIARPLPRAHKEYFTYSGKCSNP 83

1 SPYSSDTPCCFAYIARPLPRAHKEYFTYSGKCSNP 60

QY

Db

Best Local Similarity 100.0%; Pred. No. 4.5e-35; Indels 0; Gaps 0;

Matches 68; Conservative 0; Mismatches 0;

24 SPYSSDTPCCFAYIARPLPRAHKEYFTYSGKCSNP 83

1 SPYSSDTPCCFAYIARPLPRAHKEYFTYSGKCSNP 60

QY

Db

84 YINSLEMS 91

61 YINSLEMS 68

QY

Db

RESULT 14

US-10-622-134-11

; Sequence 11, Application US/10622134

; GENERAL INFORMATION:

; APPLICANT: WILLIAMS, TIMOTHY J.

; JOSE, PETER J.

; GRIFFITHS-JOHNSON, DAVID A.

; HSUAN, JOHN J.

; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHVE P.C.

; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/622,134

; FILING DATE: 18-Jul-2003

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/291,038

; FILING DATE: 14-Apr-1999

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US/08/615,232A

; FILING DATE: 13-AUG-1996

; APPLICATION NUMBER: GB 9318984

; FILING DATE: 14-SEP-1993

; APPLICATION NUMBER: GB 9408602

; FILING DATE: 29-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 550-32

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 68 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

; US-10-622-134-11

; Query Match

; Best Local Similarity 100.0%; Pred. No. 4.5e-35; Indels 0; Gaps 0;

; Mismatches 0; Conservative 68;

; 24 SPYSSDTPCCFAYIARPLPRAHKEYFTYSGKCSNP 83

; 1 SPYSSDTPCCFAYIARPLPRAHKEYFTYSGKCSNP 60

; QY

; Db

84 YINSLEMS 91  
 |||||  
 61 YINSLEMS 68

SULT 15  
 -10-332-038A-2  
 Sequence 2, Application US/10332038A  
 GENERAL INFORMATION:  
 APPLICANT: Gryphon Therapeutics, Inc.  
 APPLICANT: Offord, Robin  
 APPLICANT: Gaetner, Hubert  
 APPLICANT: Hartley, Oliver  
 TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use  
 FILE REFERENCE: 03504.271  
 CURRENT APPLICATION NUMBER: US/10/332,038A  
 CURRENT FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: US 60/217,683  
 PRIOR FILING DATE: 2000-07-12  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 2  
 LENGTH: 68  
 TYPE: PRT  
 ORGANISM: Homo Sapiens  
 -10-332-038A-2

Query Match 78.2%; Score 374; DB 6; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-35;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 SPYSSDTTCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNQVCANPEKKWVE 83  
 |||||  
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84 YINSLEMS 91  
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 61 YINSLEMS 68

arch completed: December 16, 2003, 15:47:23  
 b time : 13.4262 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

! protein - protein search, using sw model

in on: December 16, 2003, 15:36:20 : Search time 14.4208 Seconds  
(without alignments)  
266.996 Million cell updates/sec

title: US-09-920-137A-8  
length score: 478  
sequence: 1 MKVSAARLAVILLATATCAP.....VCANPEKKWVREINSLEMS 91

scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

sarched: 328717 seqs, 42310858 residues

total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	478	100.0	91	1	US-08-347-492B-12
2	478	100.0	91	1	US-08-375-346A-5
3	478	100.0	91	2	US-08-633-682-3
4	478	100.0	91	2	US-08-421-144A-8
5	478	100.0	91	2	US-08-798-143-12
6	478	100.0	91	2	US-08-467-123B-5
7	478	100.0	91	3	US-08-936-772-3
8	478	100.0	91	3	US-08-836-922-14
9	478	100.0	91	3	US-09-395-918-3
10	478	100.0	91	4	US-09-230-371A-25
11	478	100.0	91	4	US-09-639-881-14
12	472	98.7	91	1	US-08-480-449-21
13	472	98.7	91	2	US-08-660-542-21
14	472	98.7	91	4	US-08-679-493A-155
15	472	98.7	91	4	US-08-479-603-21
16	472	98.7	91	4	US-08-939-107-21
17	469	98.1	90	3	US-09-230-637-40
18	397	83.1	91	4	US-08-679-493A-156
19	393	82.2	91	2	US-08-633-682-5
20	393	82.2	91	3	US-08-936-772-5
21	393	82.2	91	3	US-09-395-918-5
22	374	78.2	68	2	US-08-936-387-1
23	374	78.2	68	2	US-08-615-232A-11
24	374	78.2	68	3	US-08-470-323-11
25	374	78.2	68	3	US-08-836-922-1
26	374	78.2	68	3	US-09-141-833-1
27	374	78.2	68	4	US-09-639-881-1

Sequence 2, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 13, Appli  
Sequence 20, Appli  
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Sequence 5, Appli  
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Sequence 16, Appli  
Sequence 5, Appli  
Sequence 2, Appli  
Sequence 18, Appli  
Sequence 14, Appli  
Sequence 14, Appli

## ALIGNMENTS

RESULT 1  
US-08-347-492B-12  
; Sequence 12, Application US/08347492B  
; Patent No. 5602008  
; GENERAL INFORMATION:  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
; TITLE OF INVENTION: PRODUCTION AND USES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,492B  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/303,241  
; FILING DATE: 07-SEP-1994  
; APPLICATION NUMBER: 08/320,011  
; FILING DATE: 05-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 91 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: GI 134510  
; US-08-347-492B-12

Query Match 100.0%; Score 478; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60

61 AVVFTRKNQVCANPEKKWVREYINSLEMS 91  
61 AVVFTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 2  
3-08-375-346A-5  
Sequence 5, Application US/08375346A  
Patent No. 5605817  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig G.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
TITLE OF INVENTION: ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,346A  
FILING DATE: 19-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0026 US  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 855-0572  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
S-08-375-346A-5

Query Match 100.0%; Score 478; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60

y 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
b 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60

QY 61 AVVFTRKNQVCANPEKKWVREYINSLEMS 91  
DB 61 AVVFTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 3  
US-08-633-682-3  
Sequence 3, Application US/08633682  
Patent No. 5840544  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,682  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0063 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: GI 134510  
US-08-633-682-3

Query Match 100.0%; Score 478; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60

QY 61 AVVFTRKNQVCANPEKKWVREYINSLEMS 91  
DB 61 AVVFTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 4  
US-08-421-144A-8  
Sequence 8, Application US/08421144A  
Patent No. 5874211  
GENERAL INFORMATION:  
APPLICANT: BANDMAN, OLGA  
APPLICANT: COLEMAN, ROGER  
APPLICANT: STUART, SUSAN G.  
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:



ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,144A  
FILING DATE: 13-APR-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF-0031 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

-08-421-144A-8

Query Match 100.0%; Score 478; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIALTALCAPASAPSYSDTTPCCFYAIARPLPRAHKEYFYTSKCSNP 60  
1 MKVSAARLAVILIALTALCAPASAPSYSDTTPCCFYAIARPLPRAHKEYFYTSKCSNP 60

61 AVFVTRKQVCANPEKKWREYINSLEMS 91  
61 AVFVTRKQVCANPEKKWREYINSLEMS 91

RESULT 5

Sequence 12, Application US/08798143  
Patent No. 5936068  
GENERAL INFORMATION:  
APPLICANT: Wilde, Craig G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
TITLE OF INVENTION: PRODUCTION AND USES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798.143  
FILING DATE: 10-FEB-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/347,492  
FILING DATE: 29-NOV-1994  
APPLICATION NUMBER: 08/303,241  
FILING DATE: 07-SEP-1994  
APPLICATION NUMBER: 08/320,011  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 134510  
US-08-798-143-12

Query Match 100.0%; Score 478; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIALTALCAPASAPSYSDTTPCCFYAIARPLPRAHKEYFYTSKCSNP 60  
DB 1 MKVSAARLAVILIALTALCAPASAPSYSDTTPCCFYAIARPLPRAHKEYFYTSKCSNP 60

QY 61 AVFVTRKQVCANPEKKWREYINSLEMS 91  
DB 61 AVFVTRKQVCANPEKKWREYINSLEMS 91

RESULT 6

US-08-467-123B-5  
Sequence 5, Application US/08467123B  
Patent No. 5945506  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig C.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
TITLE OF INVENTION: ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,123B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/375,346  
FILING DATE: 19-JAN-1995  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV  
TELECOMMUNICATION INFORMATION:

Tue Dec 16 15:54:10 2003

TELEPHONE: 415-555-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
-08-467-123B-5

Query Match 100.0%; Score 478; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

SULT 7  
-08-936-772-3  
Sequence 3, Application US/08936772  
Patent No. 6015883  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
COMPUTER: IBM Compatible  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/936,772  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/633,682  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0063 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-835-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: GI 134510  
S-08-936-772-3

Query Match 100.0%; Score 478; DB 3; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60  
DB 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60  
QY 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
DB 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
RESULT 8  
US-08-836-922-14  
; Sequence 14, Application US/08836922  
; Patent No. 6159711  
; GENERAL INFORMATION:  
; APPLICANT: INNES PROUDFOOT, AMANDA ELIZABETH  
; APPLICANT: WELLS, TIMOTHY NIGEL CARL  
; TITLE OF INVENTION: RANTES PEPTIDE AND FRAGMENTS AND  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,922  
; FILING DATE: 23-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9424835.8  
; FILING DATE: 08-DEC-1994  
; APPLICATION NUMBER: GB 9512319.6  
; FILING DATE: 16-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 1430-163  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4011  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 91 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-836-922-14

Query Match 100.0%; Score 478; DB 3; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60  
DB 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60  
QY 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
DB 61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 9  
US-09-395-918-3

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Sequence 3, Application US/09395918
Patent No. 6238666
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: DNA ENCODING RANTES HOMOLOG FROM PROSTATE
FILE REFERENCE: PF-0063 US
CURRENT APPLICATION NUMBER: US/09/395,918
CURRENT FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: GenBank: GI 134510
3-09-395-918-3

Query Match 100.0%; Score 478; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60
1 MKVSAARLAVILIATALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60
61 AVFVTRKNQVCANPEKKWREYINSLEMS 91
61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

:RESULT 10
:09-230-371A-25
Sequence 25, Application US/09230371A
Patent No. 6348596
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 91
TYPE: PRT
ORGANISM: Human
3-09-230-371A-25

Query Match 100.0%; Score 478; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60
1 MKVSAARLAVILIATALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60
61 AVFVTRKNQVCANPEKKWREYINSLEMS 91
61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

:RESULT 11
:09-639-881-14
Sequence 14, Application US/09639881
Patent No. 6555165
GENERAL INFORMATION:
APPLICANT: INNES PROUDFOOT, AMANDA ELIZABETH
APPLICANT: WELLS, TIMOTHY NIGEL CARL
TITLE OF INVENTION: RANTES PEPTIDE AND FRAGMENTS AND
TITLE OF INVENTION: COMPOSITIONS COMPRISING IT FOR TREATMENT OF INFLAMMATION
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/639,881
FILING DATE: 17-AUG-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,922
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9424835.8
FILING DATE: 08-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9512319.6
FILING DATE: 16-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION/DOCKET NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4011
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-639-881-14

Query Match 100.0%; Score 478; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60
1 MKVSAARLAVILIATALCAPASAPSYSDTTCCCFAYIARPLPRAHIKEYFTSGKCSNP 60
61 AVFVTRKNQVCANPEKKWREYINSLEMS 91
61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

:RESULT 12
US-08-480-449-21
Sequence 21, Application US/08480449
Patent No. 5688927
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
```

us-09-920-137a-8.ra1

Tue Dec 16 15:54:10 2003

CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,449  
FILING DATE:  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 27866/32779  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "RANTES"

3-08-480-449-21  
Query Match 98.7%; Score 472; DB 1; Length 91;  
Best Local Similarity 98.9%; Pred. No. 5.1e-47;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
/ 1 MKVSAARLAVILIALTALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
/ 1 MKVSAARLAVILIALTALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
/ 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91  
/ 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

RESULT 13  
S-08-660-542-21  
Sequence 21, Application US/08660542  
Patent No. 5932703  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE  
TITLE OF INVENTION: ANALOGS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murtay & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,542  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/558,658  
FILING DATE: 16-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,620  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 27866/33318  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "RANTES"  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..68  
/ 1 MKVSAARLAVILIALTALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
/ 1 MKVSAARLAVILIALTALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
/ 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91  
/ 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

Query Match 98.7%; Score 472; DB 2; Length 91;  
Best Local Similarity 98.9%; Pred. No. 5.1e-47;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
/ 1 MKVSAARLAVILIALTALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
/ 1 MKVSAARLAVILIALTALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
/ 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91  
/ 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

RESULT 14  
US-08-679-493A-155  
Sequence 155, Application US/08679493A  
Patent No. 6303295  
GENERAL INFORMATION:  
APPLICANT: Taylor, Echan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A  
CURRENT FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203  
PRIOR FILING DATE: 1995-07-14  
PRIOR APPLICATION NUMBER: 60/003,112  
PRIOR FILING DATE: 1995-09-01  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 155  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-679-493A-155

Query Match 98.7%; Score 472; DB 4; Length 91;  
Best Local Similarity 98.9%; Pred. No. 5.1e-47;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
/ 1 MKVSAARLAVILIALTALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
/ 1 MKVSAARLAVILIALTALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFTYSGKCSNP 60  
/ 61 AVFVTRKNQVCANPEKKWREYINSLEMS 91

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Tue Dec 16 15:54:10 2003

61 AVFVTRKQVNCANPEKKVREYINSLEMS 91

SULT 15  
-08-479-603-21  
Sequence 21, Application US/08479603  
Patent No. 6320023  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,603  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 27866/32780  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "RANTES"  
-08-479-603-21

Query Match 98.7%; Score 472; DB 4; Length 91;  
Best Local Similarity 98.9%; Pred.No. 5.1e-47;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 MKVSAARLAVILIALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
1 MKVSAARLAVILIALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
61 AVFVTRKQVNCANPEKKVREYINSLEMS 91  
61 AVFVTRKQVNCANPEKKVREYINSLEMS 91

Search completed: December 16, 2003, 15:40:18  
Job time: 15.4208 secs

GenCore version 5.1.6  
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protein - protein search, using sw model

n on: December 16, 2003, 15:36:20 ; Search time 13.5738 Seconds  
(without alignments)  
551.810 Million cell updates/sec

file: US-09-920-137a-7

effect score: 486

quence: 1 MKLCTVLSLLMLVAAFCSF.....VCADPSESWSQVYVDLELN 92

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283308 seqs, 96168682 residues

total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

tabase : PIR 76:\*\*

1: PIR1:\*\*

2: PIR2:\*\*

3: PIR3:\*\*

4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	92	1 A31767	macrophage inflamm
2	409	84.2	92	2 I46730	immune activation
3	390	80.2	92	2 C30522	macrophage inflamm
4	320.5	65.9	92	2 A23393	macrophage inflamm
5	320	65.8	93	2 B35673	LD78-beta protein
6	303.5	62.4	92	2 I52322	macrophage inflamm
7	300.5	61.8	92	2 A30574	macrophage inflamm
8	263	54.1	50	2 C60407	monocyte adherence
9	245.5	50.5	91	1 A28815	monocyte chemoattr
10	242.5	49.9	91	1 A46539	monocyte chemoattr
11	197.5	40.6	148	1 S07723	immediate-early se
12	192.5	39.6	109	2 A54678	monocyte chemoattr
13	185.5	38.2	148	1 A30209	PDGF-inducible JE
14	183.5	37.8	120	2 I48147	monocyte chemoattr
15	180.5	37.1	99	2 J23136	monocyte chemoattr
16	178.5	36.7	97	2 J24912	etaxin precursor
17	174.5	35.9	125	2 I46857	monocyte chemoattr
18	172.5	35.5	99	1 A39296	monocyte chemoattr
19	172.5	35.5	99	2 J23336	monocyte chemoattr
20	170.5	35.5	99	2 A60299	monocyte chemoattr
21	170.5	35.1	99	2 J25295	monocyte chemoattr
22	167.5	34.5	99	2 J24177	monocyte chemoattr
23	167	34.4	120	2 J26177	lymphocyte and mon
24	161	33.1	96	2 J24278	etaxin precursor
25	161	33.1	96	2 I48099	etaxin precursor
26	141.5	29.1	97	2 A48093	monocytic cytokine
27	137.5	28.3	96	2 A37236	I-309 protein prec
28	131.5	27.1	116	2 I49555	gene C10 protein -
29	123.5	25.4	52	2 B60407	monocyte adherence

#### ALIGNMENTS

##### RESULT 1

A31767

macrophage inflammatory protein 1-beta precursor [validated] - human  
N:Alternate names: cytokine HC21; G-26 protein; H400 homolog; lymphocyte activation ge  
protein 2 (Act-2); T-cell activation protein gamma  
C:Species: Homo sapiens (man)  
C>Date: 07-Jun-1990 #sequence revision 29-May-1998 #text change 15-Sep-2000  
C:Accession: JH0319; A40978; A31767; A37411; B30574; B45817; D30552  
R:Baikaras, E.; Roman-Roman, S.; Jitsukawa, S.; Genevee, C.; Mechiche, S.; Viegas-Pegu  
R:Napolitano, M.; Modi, W.S.; Cevario, S.J.; Gharra, J.R.; Seunaez, H.N.; Leonard, W.J  
Mol. Immunol. 27, 1091-1102, 1990  
A:Title: Cloning and expression of a lymphocyte activation gene (LAG-1).  
A:Reference number: JH0319; MUID:91061800; PMID:2247088  
A:Accession: JH0319  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-92 <BAI>  
A:Cross-references: GB:X53682; NID:G34217; PIDN:CAA37723.1; PID:G34218  
A:Experimental source: natural killer cell, strain CD3-CD2+, F5, 511E5  
R:Napolitano, M.; Modi, W.S.; Cevario, S.J.; Gharra, J.R.; Seunaez, H.N.; Leonard, W.J  
Biol. Chem. 266, 17531-17536, 1991  
A:Title: The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/tax responsiv  
A:Reference number: A40978; MUID:91373378; PMID:1894635  
A:Accession: A40978  
A:Molecule type: DNA  
A:Residues: 1-14, 'S', 16-69, 'G', 71-92 <NAP>  
A:Cross-references: GB:M69201; NID:G178021  
A>Note: 15-Ala was also found  
R:Lipes, M.A.; Napolitano, M.; Jeang, K.T.; Chang, N.T.; Leonard, W.J.  
Proc. Natl. Acad. Sci. U.S.A. 85, 9704-9709, 1988  
A:Title: Identification, cloning, and characterization of an immune activation gene.  
A:Reference number: A31767; MUID:89071764; PMID:2462251  
A:Accession: A31767  
A:Molecule type: mRNA  
A:Residues: 1-92 <LIP>  
A:Cross-references: GB:J04130; NID:G178017; PIDN:AAA51576.1; PID:G178018  
R:Chang, H.C.; Reinherz, E.L.  
Eur. J. Immunol. 19, 1045-1051, 1989  
A:Title: Isolation and characterization of a cDNA encoding a putative cytokine which i  
A:Reference number: A37411; MUID:89325421; PMID:2568930  
A:Accession: A37411  
A:Molecule type: mRNA  
A:Residues: 1-92 <CHA>  
A:Cross-references: GB:X16166; NID:G32035; PIDN:CAA34291.1; PID:G32036  
R:Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.  
J. Immunol. 142, 1582-1590, 1989  
A:Title: Mitogenic activation of human T cells induces two closely related genes which  
A:Reference number: A30574; MUID:89140347; PMID:2521882  
A:Accession: B30574  
A:Molecule type: mRNA  
A:Residues: 1-19, 'L', 21-92 <ZIP>  
A:Cross-references: GB:M25316; NID:G602454; PIDN:AAA57256.1; PID:G602455  
R:Miller, M.D.; Hata, S.; Malefyt, R.D.W.; Krangel, M.S.

30 110.5 22.7 101 2 S42496  
31 110 22.6 92 2 S24236  
32 108.5 22.3 72 2 A55984  
33 108.5 22.3 103 2 A53096  
34 107.5 22.1 114 1 ETHUL  
35 98.5 20.3 95 2 JN0841  
36 96.5 19.9 99 2 A37034  
37 94.5 19.4 101 2 I46871  
38 90.5 18.6 101 2 I48148  
39 80 16.5 114 1 ETMSL  
40 78.5 16.2 103 2 A26736  
41 78.5 16.2 103 2 I50417  
42 72.5 14.9 100 2 JH0200  
43 72.5 14.9 528 2 S70295  
44 71.5 14.7 93 2 G01540  
45 70.5 14.5 89 2 A53497

interleukin-8 prec  
TCA3 protein - mou  
monocyte chemotact  
interleukin-8 prec  
lymphotactin precu  
interleukin-8 - do  
interleukin-8 prec  
interleukin-8 - ra  
Neutrophil attract  
lymphotactin precu  
transformation-ind  
RSV-induced protei  
macrophage inflamm  
probable membrane  
cytokine SDF-1-bet  
pre-B-cell growth-

Immunol. 143, 2907-2916, 1989  
 Title: A novel polypeptide secreted by activated human T lymphocytes.  
 Reference number: A45817; MUID:90038522; PMID:2809212  
 Accession: B45817  
 Molecule type: mRNA  
 Residues: 7-55, 'I', 57-79, 'T', 81-92 <MIL>  
 Cross-references: GB:M57503; NID:G533212; PIDN:AAA36752.1; PID:G533212  
 Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
 Immunol. 142, 679-687, 1989  
 Title: A family of small inducible proteins secreted by leukocytes are members of a novel family of various activation processes.  
 Reference number: A30552; MUID:89093958; PMID:2521353  
 Accession: D30552  
 Molecule type: mRNA  
 Residues: 1-39, 'REAS', 46-92 <BRO>  
 Cross-references: GB:M23502; NID:G533212; PIDN:AAA36656.1; PID:G533213  
 Clore, G.M.; Lodi, P.J.; Garrett, D.S.; Gronenborn, A.M.  
 Submitted to the Brookhaven Protein Data Bank, January 1994  
 Reference number: A52206; PDB:1HUM  
 Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue  
 Comment: This protein is secreted by activated lymphocytes and monocytes. It is bound  
 Genetics:  
 Gene: GDB:LAG1  
 Cross-references: GDB:127451; OMIM:153335  
 Map position: 17q21-17q21  
 Introns: 26/1, 64/2  
 Superfamily: macrophage inflammatory protein  
 Keywords: chemotaxis; cytokine; inflammation  
 1-23/Domain: signal sequence #status predicted <SIG>  
 24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>  
 34-58/Disulfide bonds: #status experimental  
 Query Match 100.0%; Score 486; DB 1; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-45;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Y 1 MKLCVTVLSLLMLVAAPGSPALSPMGSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 b 1 MKLCVTVLSLLMLVAAPGSPALSPMGSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 Y 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 b 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 RESULT 2  
 46730  
 Immune activation gene 2 - rabbit  
 Species: Oryctolagus cuniculus (domestic rabbit)  
 Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 16-Jul-1999  
 Accession: I46730  
 Mori, S.; Goto, K.; Goto, F.; Murakami, K.; Ohkawata, S.; Yoshinaga, M.  
 Int. Immunol. 6, 149-156, 1994  
 Title: Dynamic changes in mRNA expression of neutrophils during the course of acute in  
 vitation  
 Reference number: I46730; MUID:94198229; PMID:8148323  
 Accession: I46730  
 Status: preliminary; translated from GB/EMBL/DBJ  
 Molecule type: mRNA  
 Residues: 1-92 <MOB>  
 Cross-references: GB:D17402; NID:G599577; PIDN:BAA04226.1; PID:G599578  
 Superfamily: macrophage inflammatory protein  
 Query Match 84.2%; Score 409; DB 2; Length 92;  
 Best Local Similarity 82.6%; Pred. No. 4.6e-37;  
 Matches 76; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
 2y 1 MKLCVTVLSLLMLVAAPGSPALSPMGSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 Db 1 MKLCVTVLSLLMLVAAPGSPALSPMGSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 2y 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 Db 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

## RESULT 3

C30552  
 macrophage inflammatory protein 1-beta precursor - mouse  
 Alternate names: H400; SIS gamma; T-cell activation protein gamma  
 Species: Mus musculus (house mouse)  
 Date: 28-Aug-1989 #sequence\_revision 28-Aug-1989 #text\_change 16-Jul-1999  
 Accession: C30552; JLO088; PS0304; S22042  
 Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
 J. Immunol. 142, 679-687, 1989  
 Title: A family of small inducible proteins secreted by leukocytes are members of a  
 s of various activation processes.  
 Reference number: A30552; MUID:89093958; PMID:2521353  
 Accession: C30552  
 Molecule type: mRNA  
 Residues: 1-92 <BRO>  
 Cross-references: GB:M23503; NID:G533244; PIDN:AAA40148.1; PID:G533245  
 R;Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; M  
 J. Exp. Med. 168, 2251-2259, 1988  
 Title: Resolution of the two components of macrophage inflammatory protein 1, and c  
 A;Reference number: JLO088; MUID:89067830; PMID:3058856  
 Accession: JLO088  
 Molecule type: mRNA  
 Residues: 1-92 <SHE>  
 Cross-references: GB:M35590; NID:G199696; PIDN:AAA39708.1; PID:G199697  
 Accession: PS0304  
 Molecule type: protein  
 Residues: 24-33, 'XX', 36, 'X', 38 <SH2>  
 Daubersies, P.; Lepretre, F.; Baillieu, B.; Grove, M.; Pragnell, I.; Plumb, M.  
 submitted to the EMBL Data Library, October 1991  
 Description: Sequence of the murine macrophage inflammatory protein 1b gene.  
 Reference number: S22042  
 Accession: S22042  
 Status: preliminary  
 Molecule type: DNA  
 Residues: 1-92 <DAU>  
 Cross-references: EMBL:X62502; NID:G53126; PIDN:CAA44364.1; PID:G53127  
 Comment: This protein is a monokine.  
 Genetics:  
 Introns: 26/1, 64/2  
 Superfamily: macrophage inflammatory protein  
 Keywords: glycoprotein  
 1-23/Domain: signal sequence #status predicted <SIG>  
 F;24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>  
 F;76/Binding site: carbohydrate (Aen) (covalent) #status predicted  
 Query Match 80.2%; Score 390; DB 2; Length 92;  
 Best Local Similarity 76.1%; Pred. No. 5.1e-35;  
 Matches 70; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MKLCVTVLSLLMLVAAPGSPALSPMGSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 Db 1 MKLCVTVLSLLMLVAAPGSPALSPMGSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 QY 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 Db 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 RESULT 4  
 A32393  
 macrophage inflammatory protein-1-alpha precursor - mouse  
 Alternate names: heparin-binding chemotaxis protein; L2G25B protein; SCI/MIP-1a; SIS  
 Species: Mus musculus (house mouse)  
 Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 16-Jul-1999  
 Accession: S11685; A32393; S04533; A53885; A30552; PS0303; A27596; I56104  
 R;Grove, M.; Lowe, S.; Graham, G.; Pragnell, I.; Plumb, M.  
 Nucleic Acids Res. 18, 5561, 1990  
 Title: Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammato  
 Reference number: S11685; MUID:91016858; PMID:2216738  
 Accession: S11685  
 Molecule type: DNA

Residues: 1-92 <GRO>  
 Cross-references: EMBL:X53372; NID:G54062; PIDN:CAA37452.1; PID:G297531  
 Note: the authors' translation of the nucleotide sequence differs at several positions  
 Kwon, B.S.; Weissman, S.M.  
 J. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
 Title: cDNA sequence of two inducible T-cell genes.  
 Reference number: A32393; MUID:89184547; PMID:2784565  
 Accession: A32393  
 Molecule type: mRNA  
 Residues: 1-92 <KNO>  
 Cross-references: GB:J04491; NID:G201524; PIDN:AAA40304.1; PID:G201525  
 Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.;  
 Exp. Med. 167, 1939-1944, 1988  
 Title: Cloning and characterization of a cDNA for murine macrophage inflammatory prote  
 Reference number: S04533; MUID:88258380; PMID:3290382  
 Accession: S04533  
 Molecule type: mRNA  
 Residues: 1-48, 'E', '50-90', 'I', '92' <DA2>  
 Cross-references: EMBL:X12531  
 Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue 9  
 Note: the sequence has been corrected in reference A53885  
 Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.;  
 Exp. Med. 170, 2189, 1989  
 Reference number: A53885  
 Contents: eratum  
 Accession: A53885  
 Molecule type: mRNA  
 Residues: 1-92 <DAV>  
 Cross-references: EMBL:X12531; NID:G53122; PIDN:CAA31047.1; PID:G53123  
 Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
 Immunol. 142, 679-687, 1989  
 Title: A family of small inducible proteins secreted by leukocytes are members of a ne  
 of various activation processes  
 Reference number: A30552; MUID:89093958; PMID:2521353  
 Accession: A30552  
 Molecule type: mRNA  
 Residues: 1-21, 'I', '23-61', 'A', '63-92' <BRO>  
 Cross-references: EMBL:X533240; PIDN:AAA40146.1; PID:G533241  
 Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Mas  
 Exp. Med. 168, 2251-2259, 1988  
 Title: Resolution of the two components of macrophage inflammatory protein 1, and clon  
 Reference number: J06088; MUID:89067830; PMID:3058856  
 Accession: P80303  
 Molecule type: mRNA  
 Residues: 24-33, 'XX', '36-54' <SHE>  
 Wolpe, S.D.; Davatelis, G.; Sherry, B.; Beutler, B.; Hesse, D.G.; Nguyen, H.T.; Moldaw  
 Exp. Med. 167, 570-581, 1988  
 Title: Macrophages secrete a novel heparin-binding protein with inflammatory and neut  
 Reference number: A27536; MUID:88154745; PMID:3279154  
 Accession: A27596  
 Molecule type: protein  
 Residues: 24-33, 'XX', '36-42' <WOL>  
 Note: 26-Met, 30-Pro, and 39-Thr were also found  
 Widmer, U.; Yang, Z.; van Deventer, S.; Manogue, K.R.; Sherry, B.; Cerami, A.  
 Immunol. 146, 4031-4040, 1991  
 Title: Genomic structure of murine macrophage inflammatory protein-1-alpha and conserv  
 Reference number: I56104; MUID:91237116; PMID:2033269  
 Accession: I56104  
 Status: preliminary; translated from GB/EMBL/DBJ  
 Molecule type: DNA  
 Residues: 1-92 <RES>  
 Cross-references: GB:M73061; NID:G195694; PIDN:AAA39707.1; PID:G195695  
 Comment: this protein is a monokine.  
 Genetics:  
 Introns: 23/3; 26/1; 63/2  
 Superfamily: macrophage inflammatory protein  
 Keywords: heparin binding  
 1-23/Domain: signal sequence #status predicted <SIG>  
 24-92/Product: macrophage inflammatory protein #status experimental <MAT>  
 Query Match 65.9%; Score 320.5; DB 2; Length 92;  
 Best Local Similarity 60.9%; Pred. No. 1.6e-27;  
 Matches 56; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 1 MKLCVTVLSLLMLVAAPFCSPALAPMGSDPTACCFSTARKLPNPNFVVDYETSSLC50 60  
 Db 1 MKVSTTAAVLCTMTLCTMVFSPYAGADTPTACCFSTARKLPNPNFVVDYETSSLC50 59  
 QY 61 PAVVFTQKRSKQVCADPSESVMQVQVYVDLELN 92  
 Db 60 PGVIFLTRGRQVCADPSESVMQVQVYVDLELN 91  
 RESULT 5  
 LD78-beta protein precursor - human  
 N:Alternate names: macrophage inflammatory protein homolog GOS19-2; small inducible cy  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: B35673; B30412; S10157; B30908  
 R:Nakao, M.; Nomiya, H.; Shimada, K.  
 Mol. Cell. Biol. 10, 3646-3658, 1990  
 A:Title: Structures of human genes coding for cytokine LD78 and their expression.  
 A:Reference number: A35673; MUID:90287155; PMID:1694014  
 A:Accession: B35673  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-93 <NAK>  
 A:Cross-references: GB:D90145; NID:G219907; PIDN:BAA14173.1; PID:G219908  
 R:Blum, S.; Forsdyke, R.E.; Forsdyke, D.R.  
 DNA Cell Biol. 9, 589-602, 1990  
 A:Title: Three human homologs of a murine gene encoding an inhibitor of stem cell prol  
 A:Reference number: A30412; MUID:91103879; PMID:2271120  
 A:Accession: B30412  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-93 <BLU>  
 A:Cross-references: GB:M24110; GB:M32338; NID:G182848; PIDN:AAA35859.1; PID:G182849  
 R:Irving, S.G.; Ziffl, P.F.; Balke, J.; McBride, O.W.; Morton, C.C.; Burd, P.R.; Sieb  
 Nucleic Acids Res. 18, 3261-3270, 1990  
 A:Title: Two inflammatory mediator cytokine genes are closely linked and variably ampli  
 A:Reference number: S10157; MUID:90287702; PMID:1972563  
 A:Accession: S10157  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-93 <IRV>  
 A:Cross-references: EMBL:X52149; NID:G34750; PIDN:CAA36397.1; PID:G296666  
 C:Comment: This protein is a member of a "small inducible" or "activation specific" ge  
 C:Genetics:  
 A:Gene: GDB:SCYA4  
 A:Cross-references: GDB:120369; OMIM:182284  
 A:Map position: 17q11-17q21  
 A:Introns: 26/1; 64/2  
 C:Superfamily: macrophage inflammatory protein  
 C:Keywords: cytokine  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-93/Product: LD78-beta protein #status predicted <MAT>  
 Query Match 65.8%; Score 320; DB 2; Length 93;  
 Best Local Similarity 58.7%; Pred. No. 1.8e-27;  
 Matches 54; Conservative 20; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 MKLCVTVLSLLMLVAAPFCSPALAPMGSDPTACCFSTARKLPNPNFVVDYETSSLC50 60  
 Db 1 MQVSTTAAVLCTMTLCTMVFSPYAGADTPTACCFSTARKLPNPNFVVDYETSSLC50 60  
 QY 61 PAVVFTQKRSKQVCADPSESVMQVQVYVDLELN 92  
 Db 61 PSVIFLTRGRQVCADPSESVMQVQVYVDLELN 92  
 RESULT 6  
 152322  
 macrophage inflammatory protein-talpa - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999



A;Cross-references: GB:M21121  
C;Comment: The acronym RANTES reflects the description "Regulated upon Activation, No."  
C;Genetics:  
A;Gene: GDB:SCYA5; D17S135E  
A;Cross-references: GDB:I30749; OMIM:137011  
A;Map position: 17q11.2-17q12  
C;Superfamily: macrophage inflammatory protein  
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell  
F;1-23/Domain: signal region #status predicted <SIG>  
F;24-91/Product: T-cell protein RANTES #status predicted <MAT>  
  
Query Match 50.5%; Score 245.5; DB 1; Length 91;  
Best Local Similarity 45.7%; Pred. No. 1.9e-19; Gaps 1;  
Matches 42; Conservative 23; Mismatches 26; Indels 1;  
  
Qy 1 MKLCVTVLSILLMVAFCSPALSPMGSDPPACCFSTARKLPNFVVDYETSSLCSQ 60  
b 1 MKYSAALAVITATATACAPAGSPYSSD-TTPCCFAYIARPLPRAHKIEFTYSGKSN 59

SULT 10  
6539  
nocyte chemoattractant cytokine RANTES precursor - mouse  
Alternate names: MuRantes  
Species: Mus musculus (house mouse)  
Date: 18-Jun-1993 #sequence revision 16-Aug-1996 #text\_change 22-Jun-1999  
Accession: I48875; I48539; I48854; I56970  
Danoff, T.M.; Lalley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.  
Immunol. 152, 1182-1189, 1994  
Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene  
Reference number: I48875; MUID:94132613; PMID:7507961  
Accession: I48875  
Status: preliminary; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-91 <DNA>  
Cross-references: EMBL:U02298; NID:G460090; PIDN:AAA18032.1; PID:G460091  
Schall, T.J.; Simpson, N.J.; Mak, J.Y.  
J. Immunol. 22, 1477-1481, 1992  
Title: Molecular cloning and expression of the murine RANTES cytokine: structural and  
Reference number: A46539; MUID:92269805; PMID:1376260  
Accession: A46539  
Molecule type: mRNA  
Residues: 1-18, A, 20-91 <SCH>  
Cross-references: GB:S37648; NID:G950207; PIDN:AAB22330.1; PID:G250208  
Experimental source: macrophage cell line PUS-1.8  
Note: Sequence extracted from NCBI backbone (NCBI:106768, NCBI:106770)  
Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.  
J. Cell. Biol. 14, 2914-2925, 1994  
Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking region  
Reference number: I48654; MUID:94217689; PMID:7513046  
Accession: I48654  
Status: translation not shown; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-91 <SHI>  
Cross-references: EMBL:X70675; NID:G475205; PIDN:CAA50011.1; PID:G475206  
Neilson, E.G.; Krensky, A.  
Int. Immun. 4, 220-225, 1992  
Title: Isolation and characterization of cDNA from renal tubular epithelium encoding  
Reference number: I56970; MUID:92277990; PMID:1375672  
Accession: I56970  
Status: translated from GB/EMBL/DBJ  
Molecule type: mRNA  
Residues: 1-40, 'E', 42-91 <NET>  
Cross-references: GB:M7747; NID:G200649; PIDN:AAA40029.1; PID:G200650  
Comment: This chemoattractant for monocytes but not neutrophils is an immediate-early  
Genetics:  
Introns: 26/1; 63/2  
Superfamily: macrophage inflammatory protein  
Keywords: chemotaxis; cytokine; immediate-early protein; inflammation  
1-23/Domain: signal sequence #status predicted <SIG>  
24-91/Product: monocyte chemoattractant cytokine RANTES #status predicted <MAT>  
Query Match 49.9%; Score 242.5; DB 1; Length 91;  
Best Local Similarity 48.9%; Pred. No. 4e-19;  
Matches 45; Conservative 20; Mismatches 26; Indels 1; Gaps 1;  
1 MKLCVTVLSLMLVAAPGSDPPTACCFSTARKLPNFVVDYVTSLSQ 60  
1 MKISAALTIILTAACTPAPSPYSD-TTPCCFAYLSALPRAHVKSFFVTSSKCSN 59  
61 PAVVFTQKRSKQVCADPSESWSWQYVVDLELN 92  
60 LAVVFTRRNQVCANPEKKWQVYINYLEMS 91

SULT 11  
17723  
mediate-early serum-responsive protein JE precursor - rat  
Alternate names: monocyte chemoattractant protein-1  
Species: Rattus norvegicus (Norway rat)  
CDate: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
CAccession: S07723; JN0128  
R.Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.  
Nucleic Acids Res. 18, 23-34, 1990  
A>Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential  
AReference number: S07723; MUID:90174947; PMID:2106664  
AAccession: S07723  
A.Molecule type: DNA  
A.Residues: 1-148 <TIM>  
A.Cross-references: EMBL:X17053; NID:G55530; PIDN:CAA34901.1; PID:G55531  
R.Yoshimura, T.; Takeya, M.; Takahashi, K.  
Biochem. Biophys. Res. Commun. 174, 504-509, 1991  
A>Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its  
AReference number: JN0128; MUID:91128376; PMID:1704226  
AAccession: JN0128  
A.Molecule type: mRNA  
A.Residues: 1-148 <YOS>  
A.Cross-references: GB:M57441; NID:G205333; PIDN:AAA63496.1; PID:G205334  
A.Experimental source: spleen cells  
A.Note: The authors translated the codon GAA for residue 62 as Lys and GCT for residue  
C.Genetics:  
A.Introns: 26/1; 65/2  
C.Superfamily: macrophage inflammatory protein  
F1-23/Domain: signal sequence #status predicted <SIG>  
F1-24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>  
Query Match 40.6%; Score 197.5; DB 1; Length 148;  
Best Local Similarity 41.9%; Pred. No. 4.6e-14;  
Matches 39; Conservative 20; Mismatches 33; Indels 1; Gaps 1;  
1 MKLCVTVLSLMLVAAPGSDPPTACCFSTARKLPNFVVDYVTSLSQ 59  
1 MQVSTVLGLLFTVAACSIHVLSDPDAVNPITCYSTGKWPMSRLNRYKRTSSRCP 60  
60 QPAVFTQKRSKQVCADPSESWSWQYVVDLELN 92  
61 KEAVFVTKLKEICADPNKEWQVYIRKLDQN 93

## RESULT 12

A54678  
monocyte chemotactic protein 3 precursor - human  
Alternate names: monocyte chemoattractant protein MCP-3  
C.Species: Homo sapiens (man)  
CDate: 28-Oct-1994 #sequence revision 28-Oct-1994 #text\_change 16-Jul-1999  
CAccession: A54678; JCI478; S32222  
R.Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys,  
Genomics 21, 403-408, 1994  
A>Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to  
AReference number: A54678; MUID:94375065; PMID:7916328  
AAccession: A54678  
A.Molecule type: DNA  
A.Residues: 1-109 <OPD>  
A.Cross-references: GB:X72309  
R.Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.  
Biochem. Biophys. Res. Commun. 191, 535-542, 1993  
A>Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA a  
AReference number: JCI478; MUID:93213290; PMID:8461011  
AAccession: JCI478  
A.Molecule type: mRNA  
A.Residues: 1-109 <OP2>  
A.Cross-references: GB:X72308; GB:S57464; NID:G3928270; PIDN:CAA51055.1; PID:G313708  
R.Miny, A.; Chalou, P.; Guillemot, J.C.; Kagnad, M.; Liauzun, P.; Megazin, M.; Miloux  
submitted to the EMBL Data Library, March 1993  
A.Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattr  
AReference number: S32222  
AAccession: S32222  
A.Molecule type: mRNA  
A.Residues: 1-109 <MIN>  
A.Cross-references: EMBL:X71087; NID:G288396; PIDN:CAA50405.1; PID:G288397  
C.Comment: This protein induces proteinase secretion and chemotaxis by macrophages and

Genetics:  
Gene: GDB:SCYA7, SCYA6, MCP-3  
Cross-References: GDB:138473, OMIM:159106  
Map position: 17q11-17q12  
Introns: 36/1; 75/2  
Superfamily: macrophage inflammatory protein  
Keywords: cytokine, glycoprotein, inflammation  
1-33/Domain: signal sequence #status predicted <SIG>  
34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>  
39/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.6%; Score 192.5; DB 2; Length 109;  
Best Local Similarity 38.5%; Pred. No. 1.2e-13;  
Matches 35; Conservative 22; Mismatches 33; Indels 1; Gaps 1;

1 MKLCVTVLSLLMLVAAPFCSPALSGSDPPTACCFSTARKLPNPFVVDYVE-TSSLCS 59  
11 MKASALLCLLLTAATFSPQGLAQPVGINTSTCCYRFINKPKQRLSYRTTSSHCP 70

60 QPAVVFOTKRSKQVCADPSESWSVQYVVDLE 90  
71 REAVIFTKLDEKICADPTQKQVQDMKHL 101

RESULT 13  
XGF-inducible JE glycoprotein precursor - mouse  
Species: Mus musculus (house mouse)  
Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
Accession: A30209; A44771; A30861  
Rollins, B.J.; Morrison, E.D.; Stiles, C.D.  
Cell. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988  
Title: Cloning and expression of JE, a gene inducible by platelet-derived growth factor  
Reference number: A30209; MUID:88234501; PMID:3287374  
Accession: A30209  
Molecule type: DNA  
Residues: 1-148 <ROL>  
Cross-References: GB:M19681; NID:G193486; PIDN:AAA37684.1; PID:G387168; GB:M19682  
Kawahara, R.S.; Deuel, T.F.  
Biol. Chem. 264, 679-682, 1989  
Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma  
Reference number: A44771; MUID:89093129; PMID:2910858  
Accession: A44771  
Molecule type: DNA; mRNA  
Residues: 1-148 <KA2>  
Cross-References: GB:J04467; NID:G193488; PIDN:AAA37685.1; PID:G387169  
Genetics:  
Gene: JE  
Introns: 26/1; 65/2  
Superfamily: macrophage inflammatory protein  
Keywords: cytokine, glycoprotein  
126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.2%; Score 185.5; DB 1; Length 148;  
Best Local Similarity 39.8%; Pred. No. 9e-13;  
Matches 37; Conservative 20; Mismatches 35; Indels 1; Gaps 1;

1 MKLCVTVLSLLMLVAAPFCSPALSGSDPPTACCFSTARKLPNPFVVDYVE-TSSLCS 59  
1 MQPVMMLGLLFTVAGSMHVLQAPDAVNAPLTCCYSFTSKMPSRLSYRTTSSRCP 60

60 QPAVVFOTKRSKQVCADPSESWSVQYVVDLE 92  
61 KEAVVFVKLKEVCADPKKEWQTVIKLDRN 93

RESULT 14  
monocyte chemoattractant protein-1 - guinea pig  
Species: Cavia porcellus (guinea pig)  
Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
Accession: 148147  
Yoshimura, T.

J. Immunol. 150, 5025-5032, 1993  
A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression  
A:Reference number: 148147; MUID:93267104; PMID:8496603  
A:Accession: 148147  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-120 <RES>  
A:Cross-References: GB:L04985; NID:G349820; PIDN:AAA37047.1; PID:G349821  
C:Genetics:  
A:Gene: MCP-1  
C:Superfamily: macrophage inflammatory protein

Query Match 37.8%; Score 183.5; DB 2; Length 120;  
Best Local Similarity 40.7%; Pred. No. 1.2e-12;  
Matches 37; Conservative 23; Mismatches 28; Indels 3; Gaps 3;

1 MKLCVTVLSLLMLVAAPFCSPALSGSDPPTACCFSTARKLPNPFVVDYVE-TSSLCS 59  
1 MQRSSVLLCLLVIEATFCSLLMAQPDGVTNPT-CCTTFN-KQIPKRVKGYERTISSRCP 58

60 QPAVVFOTKRSKQVCADPSESWSVQYVVDLE 90  
59 QPAVVFVKLKEVCADPTQKQVQDYIAKLD 89

RESULT 15  
JC2136  
monocyte chemoattractant protein-1 precursor - pig  
Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 16-Jul-1999  
C:Accession: JC2136; S57498  
R.Hosang, K.; Kroke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.  
Biochem. Biophys. Res. Commun. 199, 962-968, 1994  
A:Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Anal  
A:Reference number: JC2136; MUID:94183284; PMID:7510962  
A:Accession: JC2136  
A:Molecule type: mRNA  
A:Residues: 1-99 <HOS>  
A:Cross-References: GB:Z48479; NID:G683716; PIDN:CAA88370.1; PID:G683717  
R.Zach, O.  
submitted to the EMBL Data Library, July 1994  
A:Reference number: S57497  
A:Accession: S57498  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-99 <ZAC>  
A:Cross-References: EMBL:X79416; NID:G872312; PIDN:CAA55945.1; PID:G872313  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: glycoprotein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>  
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.1%; Score 180.5; DB 2; Length 99;  
Best Local Similarity 35.2%; Pred. No. 2.1e-12;  
Matches 32; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

1 MKLCVTVLSLLMLVAAPFCSPALSGSDPPTACCFSTARKLPNPFVVDYVE-TSSLCS 59  
1 MKVSAALLCLLLTAATCTCTQLAQPDAINSPTCCYLTSTKISMQRMSYRRTSSKCP 60

60 QPAVVFOTKRSKQVCADPSESWSVQYVVDLE 90  
61 KEAVIFTKIAGKEICAEFPKQKQVQDSISHL 91

Search completed: December 16, 2003, 15:40:57  
Job time : 14:5738 secs

GenCore version 5.1.6  
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protein - protein search, using sw model

on on December 16, 2003, 15:36:20 ; Search time 10.574 Seconds  
(without alignments)  
409.804 Million cell updates/sec

file: US-09-920-137A-7

efect score: 486  
quence: 1 MKLCVTVLSLLMLVAFCSP.....VCADPSESWMQEVYVDLELN 92

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tal number of hits satisfying chosen parameters: 127863

nimum DB seq length: 0  
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

tabase : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	92	1 SY04_HUMAN	P12336 h small ind
2	409	84.2	92	1 SY04_RABIT	P46632 cryptotlagus
3	394	81.1	92	1 SY04_RAT	P50230 rattus norv
4	390	80.2	92	1 SY04_MOUSE	P14097 mus musculu
5	320	65.9	92	1 SY03_MOUSE	P10855 mus musculu
6	320	65.8	93	1 SY3L_HUMAN	P16619 homo sapien
7	303.5	62.4	92	1 SY03_RAT	P50229 rattus norv
8	300.5	61.8	92	1 SY03_HUMAN	P10147 homo sapien
9	264	54.3	90	1 SY04_CHICK	Q30826 gallus gall
10	246.5	50.7	91	1 SY05_BOVIN	Q97919 bos taurus
11	245.5	50.5	91	1 SY05_HUMAN	P13501 homo sapien
12	242.5	49.9	91	1 SY05_MOUSE	P10882 mus musculu
13	238.5	49.1	91	1 SY05_SIGHI	Q12111 sigmodon hi
14	234.5	48.3	91	1 SY05_CAVPO	P97272 cavia porce
15	229	47.1	92	1 SY05_RAT	P50231 rattus norv
16	224.5	46.2	93	1 SY14_HUMAN	Q16627 homo sapien
17	210	43.2	98	1 SY18_HUMAN	P55774 h small ind
18	199	40.9	98	1 SY13_HUMAN	Q99616 homo sapien
19	197.5	40.6	148	1 SY02_RAT	P14844 rattus norv
20	192.5	39.6	99	1 SY07_HUMAN	P80098 homo sapien
21	185.5	38.2	148	1 SY02_MOUSE	P10148 mus musculu
22	184	37.9	120	1 SY16_HUMAN	Q15467 h small ind
23	183.5	37.8	120	1 SY02_CAVPO	Q08782 cavia porce
24	180.5	37.1	99	1 SY02_PIG	P42831 sus scrofa
25	179.5	36.9	97	1 E0TA_HUMAN	P51671 homo sapien
26	176.5	36.3	97	1 E0TA_RAT	P97545 rattus norv
27	174.5	35.9	99	1 SY08_HUMAN	P80075 homo sapien
28	174.5	35.9	125	1 SY02_RABIT	P28292 cryptotlagus
29	172.5	35.5	94	1 SY26_HUMAN	Q9Y258 homo sapien
30	172.5	35.5	99	1 MCPA_BOVIN	P28291 bos taurus
31	172.5	35.5	99	1 SY02_HUMAN	P13500 homo sapien
32	172.5	35.5	99	1 SY02_NACFA	Q9myn4 macaca fasc
33	170	35.0	120	1 SY23_HUMAN	P55773 homo sapien

#### ALIGNMENTS

##### RESULT 1

ID	SY04_HUMAN	STANDARD;	PRT;	92 AA.
AC	P12336; P22617; Q13704;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory			
DE	protein 1-beta) (MIP-1-beta) (T-cell activation protein 2) (ACT-2)			
DE	(PAT 744) (H400) (SIS-gamma) (Lymphocyte activation gene-1 protein)			
DE	(LAG-1) (HC21) (G-26 T lymphocyte-secreted protein).			
GN	CCL4 OR SCVA4 OR MIP1B OR LAG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89071764; PubMed=2462251;			
RA	Lipes M.A., Napolitano M., Jeang K.-T., Chang N.T., Leonard W.J.;			
RT	"Identification, cloning, and characterization of an immune			
RT	activation gene";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:9704-9708 (1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89140347; PubMed=2521882;			
RA	Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;			
RT	"Mitogenic activation of human T cells induces two closely related			
RT	genes which share structural similarities with a new family of			
RT	secreted factors";			
RL	J. Immunol. 142:1582-1590 (1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89093958; PubMed=2521353;			
RA	Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;			
RT	"A family of small inducible proteins secreted by leukocytes are			
RT	members of a new superfamily that includes leukocyte and fibroblast-			
RT	derived inflammatory agents, growth factors, and indicators of various			
RT	activation processes";			
RL	J. Immunol. 142:679-687 (1989).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91061800; PubMed=2247088;			
RA	Baixeras E., Roman-Roman S., Jitsukawa S., Genevée C., Mechiche S.;			
RT	"Cloning and expression of a lymphocyte activation gene (LAG-1)";			
RT	Mol. Immunol. 27:1091-1102 (1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RT	TISSUE=T-cell;			
RX	MEDLINE=89325421; PubMed=2568930;			
RA	Chang H.C., Reinherz E.L.;			
RT	"Isolation and characterization of a cDNA encoding a putative			
RT	cytokine which is induced by stimulation via the CD2 structure on			
RT	human T lymphocytes";			
RL	Eur. J. Immunol. 19:1045-1051 (1989).			

34	168.5	34.7	97	1	E0TA_MOUSE
35	167.5	34.5	99	1	SY08_PIG
36	166.5	34.3	99	1	SY08_BOVIN
37	166.5	34.3	113	1	SV15_HUMAN
38	164.5	33.8	94	1	VNI2_KSHV
39	164.5	33.8	101	1	SY02_CANFA
40	161	33.1	96	1	E0TA_CAVPO
41	156	32.1	70	1	REG1_BOVIN
42	152.5	31.4	119	1	SY24_MOUSE
43	150.5	31.0	119	1	SY24_HUMAN
44	146.5	30.1	97	1	SY07_MOUSE
45	146.5	30.1	97	1	SY08_MOUSE

P48298	mus musculu
P49873	sus scrofa
Q09141	bos taurus
Q16663	homo sapien
Q98157	kaposi's sa
P22203	canis famil
P80325	cavia porce
P82943	bos taurus
Q9JKCO	mus musculu
Q00175	homo sapien
Q03366	mus musculu
Q9Z121	mus musculu

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[6]
SEQUENCE FROM N.A.
MEDLINE=91373378; PubMed=1894635;
Napolitano M., Modi W.S., Cevalero S.J., Gnaria J.R., Seauanez H.N.,
Leonard W.J.;
"The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/Tax
responsiveness of 5' upstream sequences, and chromosomal
localization.";
J. Biol. Chem. 266:17531-17536(1991).
[7]
SEQUENCE FROM N.A.
Biren B., Fasman K., McKernan K., Nusbaum C., Richardson P.,
Lander E.;
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[8]
SEQUENCE OF 6-92 FROM N.A.
MEDLINE=90038522; PubMed=2809212;
Miller M.D., Hata S., Waal Malefyt R., Krangel M.S.;
"A novel polypeptide secreted by activated human T lymphocytes.";
J. Immunol. 143:2907-2916(1989).
[9]
RECEPTOR INTERACTION.
MEDLINE=98180363; PubMed=9521068;
Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
Napolitano M.;
"Identification of the CC chemokines TARC and macrophage inflammatory
protein-1 beta as novel functional ligands for the CCR8 receptor.";
Eur. J. Immunol. 28:582-588(1998).
[10]
FUNCTION.
MEDLINE=96106406; PubMed=8525373;
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
Lusso P.;
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major
HIV-suppressive factors produced by CD8+ T cells.";
Science 270:1811-1815(1995).
[11]
STRUCTURE BY NMR.
MEDLINE=94182137; PubMed=8134838;
Lodi P.J., Garrett D.S., Kuscewski J., Teang M.L.S., Weatherbee J.A.,
Leonard W.J., Gronenborn A.M., Clore G.M.;
"High-resolution solution structure of the beta chemokine hMIP-1 beta
by multidimensional NMR.";
Science 263:1762-1767(1994).
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.
BINDS TO CCR5 AND TO CCR8. ONE OF THE MAJOR HIV-SUPPRESSIVE
FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-BETA INDUCES A
DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2,
AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- INDUCTION: By mitogens.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
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or send an email to license@isb-sib.ch).
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EMBL; M23502; AAA36656.1; -
EMBL; M23516; AAA57256.1; -
EMBL; J04130; AAA51576.1; -
EMBL; X53683; CAA37723.1; -
EMBL; X53682; CAA37722.2; ALT SEQ.
EMBL; X16166; CAA34291.1; -
EMBL; M69203; AAB00790.1; -
EMBL; M69201; AAB00790.1; JOINED.
EMBL; M69202; AAB00790.1; JOINED.

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DR EMBL; AC003976; -: NOT ANNOTATED\_CDS.  
 DR EMBL; M57503; AAA36752.1; -  
 DR PIR; JH0319; A31767.  
 DR PDB; 1HUM; 30-APR-94.  
 DR PDB; 1HUN; 30-APR-94.  
 DR PDB; 1JEA; 03-OCT-01.  
 DR Genew; HGNC:10630; CCL4.  
 DR MIM; 182284; -  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0006003; F:chemokine activity; TAS.  
 DR GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . .; TAS.  
 DR GO; GO:0007155; P:cell adhesion; TAS.  
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.  
 DR GO; GO:0006928; P:cell-cell signaling; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0007163; P:establishment and/or maintenance of cell po. . .; TAS.  
 DR GO; GO:0006955; P:immune response; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR GO; GO:0003615; P:response to viruses; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR GO; GO:0008166; P:viral replication; TAS.  
 DR InterPro; IPR000827; CC:chemokine\_sml.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 DR KX Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.  
 FT SIGNAL 1 23  
 FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.  
 FT DISULFID 34 58 BY SIMILARITY.  
 FT DISULFID 35 74 BY SIMILARITY.  
 FT CONFLICT 5 6 T -> C (IN REF. 7).  
 FT CONFLICT 15 15 A -> S (IN REF. 6).  
 FT CONFLICT 20 20 P -> L (IN REF. 2).  
 FT CONFLICT 40 45 ARKLP -> REASS (IN REF. 3).  
 FT CONFLICT 56 56 S -> I (IN REF. 8).  
 FT CONFLICT 70 70 S -> G (IN REF. 6).  
 FT CONFLICT 80 70 S -> T (IN REF. 7 AND 8).  
 FT STRAND 29 29  
 FT STRAND 33 33  
 FT STRAND 45 47  
 FT STRAND 50 53  
 FT STRAND 63 66  
 FT STRAND 72 75  
 FT TURN 77 78  
 FT HELIX 80 92  
 SQ SEQUENCE 92 AA; 10212 MW; F2EA7CF341B0E258 CRC64;  
 Query Match 100.0%; Score 486; DB 1; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-47;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLCVTVLISLMLVAFCSPALSGSDPPTACCFSTARKLPNFVVDYETSSLCQ 60  
 Db 1 MKLCVTVLISLMLVAFCSPALSGSDPPTACCFSTARKLPNFVVDYETSSLCQ 60  
 QY 61 PAVVFQTKRSQKQVCADPSESWMQYVVDLELN 92  
 Db 61 PAVVFQTKRSQKQVCADPSESWMQYVVDLELN 92  
 RESULT 2  
 SY04\_RABIT STANDARD; PRT; 92 AA.  
 ID SY04\_RABIT  
 AC P46632;  
 DT 01-NOV-1995 (Rel. 32; Created)  
 DT 01-NOV-1995 (Rel. 32; Last sequence update)  
 DT 28-FEB-2003 (Rel. 41; Last annotation update)  
 DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory  
 DE protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).  
 DE CCL4 OR SCYA4.  
 GN Oryctolagus cuniculus (Rabbit).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
[1]
SEQUENCE FROM N.A.
STRAIN=New Zealand white;
MEDLINE=94198229; PubMed=8148323;
Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
"Dynamic changes in mRNA expression of neutrophils during the course
of acute inflammation in rabbits.";
Int. Immunol. 6:1149-1156(1994).
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES
(BY SIMILARITY).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
-----
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or send an email to license@isb-sib.ch).
-----
EMBL; D17402; BAA04226.1; -
PIR; I46730; I46730.
HSP; P13236; 1HUM.
InterPro; IPR000827; CC_chemokine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Inflammatory response; Signal.
CHAIN 1 23 BY SIMILARITY.
DISULFID 24 92 SMALL INDUCIBLE CYTOKINE A4.
DISULFID 34 58 BY SIMILARITY.
DISULFID 35 74 BY SIMILARITY.
SEQUENCE 92 AA; 10066 MW; ECBA8818D42A735C CRC64;
Query Match 84.2%; Score 409; DB 1; Length 92;
Best Local Similarity 82.6%; Pred. No. 1.9e-38;
Matches 76; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
/ 1 MKLCVTLSLLMLVAAPGSPALSPMGSDPTACCFSTARKLPNFVVDYVYETSSLCQ 60
/ 1 MKLGTVLVSVLLVAALCPALSPMGSDPTACCFSTARKLPNFVVDYVYETSSLCQ 60
/ 61 PAVVFTKRSKQVCADPSSWQVQYVVDLELN 92
/ 61 PAVVFTKRGQVCANPSSWQVQYVVDLELN 92
RESULT 3
SY04 RAT STANDARD; PRT; 92 AA.
MEDLINE=89067830; PubMed=3058856;
Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G.,
Wolpe S.D., Maslarz F., Coit D., Cerami A.;
"Resolution of the two components of macrophage inflammatory protein
Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
protein 1-beta) (MIP-1-beta).
CCL4 OR SCYA4 OR MIP1B.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=8903958; PubMed=2521353;
Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
"A family of small inducible proteins secreted by leukocytes are
members of a new superfamily that includes leukocyte and fibroblast-
derived inflammatory agents, growth factors, and indicators of various
activation processes.";
J. Immunol. 142:679-687(1989).
[3]

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SEQUENCE FROM N.A.
STRAIN=BA/2J, TISSUE=Liver;
Daubersies P., Lepretre F., Bailloul B., Grove M., Pragnell I.,
Plumb M.A.;
Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;
MEDLINE=99370037; PubMed=10438970;
Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
Blankenhorn E.P.;
"Sequence polymorphisms in the chemokines Sca1 (TCA-3), Sca2
(monocyte chemoattractant protein (MCP)-1), and Sca12 (MCP-5) are
candidates for eae7, a locus controlling susceptibility to monophasic
remitting/nonrelapsing experimental allergic encephalomyelitis.";
J. Immunol. 163:2262-2266(1999).
[5]
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; M23503; AAA40148.1; -
EMBL; M35590; AAA39708.1; -
EMBL; X62502; CAA44364.1; -
EMBL; AF128218; AAF22559.1; -
EMBL; AF128219; AAF22560.1; -
PIR; C30552; C30552.
HSP; F13236; IHUM.
MGD; MG1:98261; Ccl14.
InterPro; IPR000827; CC_chemokine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; Inflammatory response; Signal.
SIGNAL
1 23
CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.
T DISULFID 34 58 BY SIMILARITY.
T DISULFID 35 74 BY SIMILARITY.
T DISULFID 35 74
SEQUENCE 92 AA; 10168 MW; 8853FD58FDE51BAC CRC64;
Query Match 80.2%; Score 390; DB 1; Length 92;
Best Local Similarity 76.1%; Pred No. 2.4e-36;
Matches 70; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
y 1 MKLCVTVLSLLMLVAFCSPALAPMGSDPPACFSYTARKLPNFVVDYETSLCSQ 60
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b 1 MKLCVLSALLLVAACFAPGFSAPMGSDPPSCFSYTRQLHRFVMDYETSLCSK 60
y 61 PAVVFTKRSKQVADPSSEWVQEVYVDLELN 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b 61 PAVVFLTKGRQICANPSEFWVTEYMSDLELN 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 5
y03 MOUSE
D SY03 MOUSE STANDARD; PRT; 92 AA.
AC P10855; P14096;
JT 01-JUL-1989 (Rel. 11, Created)
JT 15-SEP-2003 (Rel. 14, Last sequence update)
JT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A3 precursor (CCU3) (Macrophage inflammatory
protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (L2G25B).
DE Chemotaxis protein) (L2G25B).

```

GN OS CCL3 OR SCYA3 OR MIPIA.  
 Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88258380; PubMed=3290382;  
 RA Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermesen K., Luedke C.,  
 RA Gallegos C., Coit D., Merryweather J., Cerami A.;  
 RT "Cloning and characterization of a cDNA for murine macrophage  
 RT inflammatory protein (MIP), a novel monokine with inflammatory and  
 RT chemokinetic properties.";   
 RL J. Exp. Med. 167:1939-1944 (1988).  
 RN [2]  
 RP REVISIONS.  
 RA Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermesen K., Luedke C.,  
 RA Gallegos C., Coit D., Merryweather J., Cerami A.;  
 RL J. Exp. Med. 170:2189-2189 (1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89093958; PubMed=2521353;  
 RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;  
 RT "A family of small inducible proteins secreted by leukocytes are  
 RT members of a new superfamily that includes leukocyte and  
 RT fibroblast-derived inflammatory agents, growth factors, and  
 RT indicators of various activation processes.";   
 RL J. Immunol. 142:679-687 (1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=BA/2J;  
 RX MEDLINE=91016858; PubMed=2216738;  
 RA Grove M., Lowe S., Graham G., Pragnell I., Plumb M.;  
 RT "Sequence of the murine haemopoietic stem cell inhibitor/macrophage  
 RT inflammatory protein 1 alpha gene";   
 RL Nucleic Acids Res. 18:5561-5561 (1990).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89184547; PubMed=2784565;  
 RA Kwon B.S., Weissman S.M.;  
 RT "cDNA sequences of two inducible T-cell genes.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967 (1989).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91237116; PubMed=2033269;  
 RA Widmer U., Yang Z., van Deventer S., Manogue K.R., Sherry B.,  
 RA Cerami A.;  
 RT "Genomic structure of murine macrophage inflammatory protein-1 alpha  
 RT and conservation of potential regulatory sequences with a human  
 RT homolog, LD78.";   
 RL J. Immunol. 146:4031-4040 (1991).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=BALB/CJ, DBA/2J, NOD/LTJ, SJL/J, and B10.S/J; TISSUE=Spleen;  
 RX MEDLINE=99370037; PubMed=10438970;  
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
 RA Blankenhorn E.P.;  
 RT "Sequence polymorphisms in the chemokines Sca1 (TCA-3), Sca2  
 RT (monocyte chemoattractant protein (MCP)-1), and Sca12 (MCP-5) are  
 RT candidates for eae7, a locus controlling susceptibility to monophasic  
 RT remitting/nonrelapsing experimental allergic encephalomyelitis.";   
 RL J. Immunol. 163:2262-2266 (1999).  
 RN [8]  
 RP SEQUENCE OF 24-42.  
 RX MEDLINE=88154745; PubMed=3279154;  
 RA Wolpe S.D., Davatelis G., Sherry B., Beutler B., Hesse D.G.,  
 RA Nguyen H.T., Moldawer L.L., Nathan C.F., Lowry S.F., Cerami A.;  
 RT "Macrophages secrete a novel heparin-binding protein with  
 RT inflammatory and neutrophil chemokinetic properties";   
 RL J. Exp. Med. 167:570-581 (1988).  
 CC -!- FUNCTION: MONOKINE WITH INFLAMMATORY, PYROGENIC AND CHEMOKINETIC  
 CC PROPERTIES. HAS A POTENT CHEMOTACTIC ACTIVITY FOR EOSINOPHILS.  
 CC BINDING TO A HIGH-AFFINITY RECEPTOR ACTIVATES CALCIUM RELEASE IN

```

NEUTROPHILS.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, AND PANCREAS.
-1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC)

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EMBL; M23447; AAA40146.1; -
EMBL; X12531; CAA31047.1; -
EMBL; X53372; CAA37452.1; -
EMBL; J04491; AAA40304.1; -
EMBL; M73061; AAA39707.1; -
EMBL; AF065939; AAC17506.1; -
EMBL; AF065940; AAC17507.1; -
EMBL; AF065941; AAC17508.1; -
EMBL; AF065942; AAC17509.1; -
EMBL; AF065943; AAC17510.1; -
PIR; S11685; A32393.
HSPG; P13236; IHUM.
MGD; MGI:98260; Cel3.
GO; GO:0008009; F:chemokine activity; IDA.
InterPro; IPR000827; CC_chemokine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCV; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; Inflammatory response; Signal.
SIGNAL 1 23 SMALL INDUCIBLE CYTOKINE A3.
CHAIN 24 92
DISULFID 34 57 BY SIMILARITY.
DISULFID 35 73 BY SIMILARITY.
CONFLICT 22 22 F -> L (IN REF. 3).
CONFLICT 62 62 V -> A (IN REF. 3).
SEQUENCE 92 AA; 10345 MW; 8BFF2DE7C6DEDD38 CRC64;

Query Match 65.9%; Score 320.5; DB 1; Length 92;
Best Local Similarity 60.9%; Pred. No. 1.1e-28;
Matches 56; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

1 MKLCVTVLSLMLVAFCSPALSPAGSDPTACCFSTYARKLPNRFVDFYETSLCSQ 60
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 MKVSTTALAVLLCTMTLCNQVSPAGYADPTACCFSTY-SRKIPRQIVDFYETSLCSQ 59
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

61 PAVVQFQYRSKQVADPSESVQVQVVDLELN 92
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
60 PGVIFLTKRNQICADSKETWQVYITDLELN 91
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 6
(3) HUMAN
SYL HUMAN STANDARD; PRT; 93 AA.
P16619; Q96168;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A3 like 1 precursor (Tonsillar lymphocyte
LD78 beta protein) (GO/G1 switch regulatory protein 19-2) (GOS19-2
protein) (P46 46.2)
CCL3L1 OR SCY3A11 OR GOS19-2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Blood;

```

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RX MEDLINE=90287702; PubMed=1972563;
RA Irving S.G., Zipfel P.F., Balke J., McBride O.W., Morton C.C.,
RA Burd P.R., Siebenlist U., Kelly K.;
RT "Two inflammatory mediator cytokine genes are closely linked and
RT variably amplified on chromosome 17q.";
RL Nucleic Acids Res. 18:3261-3270(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91103879; PubMed=2271120;
RA Blum S., Forsdyke R.E., Forsdyke D.R.;
RT "Three human homologs of a murine gene encoding an inhibitor of stem
RT cell proliferation.";
RL DNA Cell Biol. 9:589-602(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90287155; PubMed=1694014;
RA Nakao M., Nomiya H., Shimada K.;
RT "Structures of human genes coding for cytokine LD78 and their
RT expression.";
RL Mol. Cell. Biol. 10:3646-3658(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=B-cell, Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Gunatane P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra W.A., 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC). STRONG, TO SCY3.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X52149; CAA36397.1; -
CC EMBL; M24110; AAA35859.1; -
CC EMBL; D90145; BAA14173.1; -
CC EMBL; BC007783; AAH27883.1; -
CC EMBL; BC027888; AAH27888.1; -
CC PIR; B35673; B35673.
CC HSPG; P13236; IHUM.
CC Genew; HGNC:10628; CCL3L1.
CC MIM; 601395; -
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0008009; F:chemokine activity; NAS.
CC GO; GO:0006935; P:chemotaxis; NAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
CC InterPro; IPR000827; CC_chemokine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.

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SMART: SM00199; SCV: 1.
PROSITE: PS00472; SMALL CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; Signal.
CHAIN 1 23 SMALL INDUCIBLE CYTOKINE A3 LIKE 1.
BY SIMILARITY.
DISULFID 34 58
BY SIMILARITY.
DISULFID 35 74
BY SIMILARITY.
CONFLICT 91 91 L -> P (IN REF. 4; AAH07783).
SEQUENCE 93 AA; 10161 MW; A7A79E774006D61E CRC64;

Query Match 65.8%; Score 320; DB 1; Length 93;
Best Local Similarity 58.7%; Pred. No. 1.3e-28;
Matches 54; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

/ 1 MKLCVTVLMLVAAPCSAPALSGDPPTACFSYATKLRNPFVVDYVYETSSICSQ 60
/ 1 MKVSTAALAVLLCTMALNQVLAPLAADTTACFSYTSRQIPQNFADYFETSSQCSK 60
Y 61 PAVVFTQKRSQVQCADPSESWQVYVVDLEIN 92
b 61 PSVIFLTRGRQVQCADPSEWQVQYVVDLEIN 92

RESULT 7
Y03_RAT
D S103_RAT STANDARD; PRT; 92 AA.
C P50229;
T 01-OCT-1996 (Rel. 34, Created)
T 01-OCT-1996 (Rel. 34, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
E protein 1-alpha) (MIP-1-alpha).
E CCL3 OR SCYA3 OR MIP1A.
S Rattus norvegicus (Rat).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
X NCBI_TaxID=10116;
P SEQUENCE FROM N.A.
C TISSUE=Lung;
X MEDLINE=95298037; PubMed=7779098;
A Shi M.M., Godleski J.J., Paulauskis J.D.;
T "Molecular cloning and posttranscriptional regulation of macrophage
T inflammatory protein-1 alpha in alveolar macrophages.";
L Biochem. Biophys. Res. Commun. 211:289-295(1995).
P [2]
N SEQUENCE FROM N.A.
C STRAIN=Long Evans; TISSUE=Lung;
X MEDLINE=95238980; PubMed=772328;
A Shanley T.P., Schmal H., Friedl H.P., Jones M.L., Ward P.A.;
T "Role of macrophage inflammatory protein-1 alpha (MIP-1 alpha) in
T acute lung injury in rats.";
L J. Immunol. 154:4793-4802(1995).
P [3]
N SEQUENCE OF 24-57.
C STRAIN=Wistar;
X MEDLINE=96183056; PubMed=8607872;
A Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
T "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
T member of rat GRO/CINC3, is a predominant chemokine produced by
T lipopolysaccharide-stimulated rat macrophages in culture.";
L Biochem. Biophys. Res. Commun. 220:945-948(1996).
P [1]
N FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.
C HAS CHEMOTACTIC ACTIVITY FOR MONOCYTES, NEUTROPHILS, EOSINOPHILS,
C BASOPHILS, AND LYMPHOCYTES. REQUIRED FOR LUNG TNF-ALPHA
C PRODUCTION, NEUTROPHIL RECRUITMENT AND SUBSEQUENT LUNG INJURY AND
C MAY FUNCTION AS AN AUTOCHINE MEDIATOR FOR THE MACROPHAGE
C PRODUCTION OF TNF-ALPHA WHICH IN TURN UP-REGULATES VASCULAR
C ADHESION MOLECULES REQUIRED FOR NEUTROPHIL INFUX. THIS PROTEIN
C BINDS HEPARIN.
C [1]- SUBCELLULAR LOCATION: Secreted.
C [1]- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS).
C [1]- SIMILARITY: BELONGS TO THE INTERCINE BETA FAMILY (SMALL CYTOKINE

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C-C) (CHEMOKINE CC).
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between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
EMBL; U22414; AAA80608.1; -
EMBL; U06435; AAA36498.1; -
PIR; I52322; I52322.
HSP: P13236; 1HUM.
InterPro: IPR000827; CC chemokine sm1.
InterPro: IPR001811; Chemokine_IL8.
Pfam: PF00048; IL8; 1.
SMART; SM00199; SCV; 1.
PROSITE; PS00472; SMALL CYTOKINES_CC; 1.
CYTOKINE; Chemotaxis; Inflammatory response; Signal; Heparin-binding.
CHAIN 1 23 SMALL INDUCIBLE CYTOKINE A3.
BY SIMILARITY.
DISULFID 34 57
BY SIMILARITY.
DISULFID 35 73
BY SIMILARITY.
CONFLICT 6 6 A -> T (IN REF. 2).
CONFLICT 57 57 C -> W (IN REF. 2 AND 3).
SEQUENCE 92 AA; 10335 MW; 14E861C647F9A2EB CRC64;

Query Match 62.4%; Score 303.5; DB 1; Length 92;
Best Local Similarity 57.6%; Pred. No. 8.3e-27;
Matches 53; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

Oy 1 MKLCVTVLMLVAAPCSAPALSGDPPTACFSYATKLRNPFVVDYVYETSSICSQ 60
Db 1 MKVSTAALAVLLCTMALNQVLAPLAADTTACFSY-GRQIPKFIADYFETSSICSQ 59
Oy 61 PAVVFTQKRSQVQCADPSESWQVYVVDLEIN 92
Db 60 PGVIFLTRGRQVQCADPKEITWQVYITELEIN 91

RESULT 8
SY03_HUMAN
ID SY03_HUMAN STANDARD; PRT; 92 AA.
AC P10147;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
DE protein 1-alpha) (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha
DE protein) (GO/G1 switch regulatory protein 19-1) (GOS19-1 protein)
DE (SIS-beta) (PAT 464.1).
DE CCL3 OR SCYA3 OR GOS19-1 OR MIP1A.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86223979; PubMed=3086300;
RA Obaru K., Fukuda M., Maeda S., Shimada K.;
RT "A cDNA clone used to study mRNA inducible in human tonsillar
RT lymphocytes by a tumor promoter.";
J. Biochem. 93:885-894(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89140347; PubMed=2521882;
RA Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;
RT "Mitogenic activation of human T cells induces two closely related
RT genes which share structural similarities with a new family of
RT secreted factors.";
J. Immunol. 142:1582-1590(1989).
RN [3]

```

SEQUENCE FROM N.A.  
MEDLINE=91103879; PubMed=2271120;  
Blum S., Forsdyke R.E., Forsdyke D.R.;  
"Three human homologs of a murine gene encoding an inhibitor of stem  
cell proliferation.";  
DNA Cell Biol. 9:589-602(1990).  
[4]  
SEQUENCE FROM N.A.  
MEDLINE=90287155; PubMed=1694014;  
Nakao M., Noniyama H., Shimada K.;  
"Structures of human genes coding for cytokine LD78 and their  
expression.";  
Mol. Cell. Biol. 10:3646-3658(1990).  
[5]  
SEQUENCE OF 23-92 FROM N.A.  
Jang J.S., Kim B.E.;  
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
[6]  
SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49.  
MEDLINE=96127782; PubMed=8541527;  
Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S.,  
Czaplewski L.G., Dexter T.M., Drummond A.H., Gearing A.H.,  
Heworth C.M., Lord B.I., Mccourt M., Varley P.G., Wood L.M.,  
Edwards R.M., Lewis P.J.;  
"BB-10010: an active variant of human macrophage inflammatory protein-  
1 alpha with improved pharmaceutical properties.";  
Blood 86:4400-4408(1995).  
[7]  
SEQUENCE OF 27-40 AND 71-93, AND FUNCTION.  
MEDLINE=96106406; PubMed=8525373;  
Cocchi F., Devico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,  
Lusso P.;  
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major  
HIV-suppressive factors produced by CD8+ T cells.";  
Science 270:1811-1815(1995).  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.  
BINDS TO CCRL, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE  
FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-ALPHA INDUCES  
A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2,  
AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- INDUCTION: BY TPA OR PHA (TPA = 12-O-TETRADECANOYL PHORBOL-13  
ACETATE (TUMOR PROMOTER); PHA = PHYTOHEMAGGLUTININ (T-CELL  
MITOGEN)).  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC). STRONG, TO SCY431.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; D00044; BAA00029.1; -  
EMBL; M23452; AAA36316.1; -  
EMBL; M25315; AAA57255.1; -  
EMBL; X03754; CAA27388.1; -  
EMBL; X04018; CAA27643.1; ALT\_SEQ.  
EMBL; M21178; AAA35858.1; -  
EMBL; D90144; BAA14172.1; -  
EMBL; A2043339; AAC03539.1; -  
FIR; A35673; A30574.  
PDB; 1B50; 22-JUL-99.  
PDB; 1B53; 22-JUL-99.  
Genew; HGNC:10627; CCL3.  
MIM; 182283; -  
GO; GO:0005625; C:soluble fraction; TAS.  
GO; GO:0003800; F:antiviral response protein activity; TAS.  
GO; GO:0008009; F:chemokine activity; TAS.  
GO; GO:0004871; F:signal transducer activity; TAS.  
GO; GO:0006961; P:antibacterial humoral response (sensu Inver. . . ; TAS.

GO; GO:0006874; P:calcium ion homeostasis; TAS.  
GO; GO:0006928; P:cell motility; TAS.  
GO; GO:0007267; P:cell-cell signaling; TAS.  
GO; GO:0006935; P:chemotaxis; TAS.  
GO; GO:0006887; P:exocytosis; TAS.  
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.  
GO; GO:0006355; P:immune response; TAS.  
GO; GO:0008954; P:inflammatory response; TAS.  
GO; GO:0007011; P:regulation of cytoskeleton; TAS.  
GO; GO:0007165; P:signal transduction; TAS.  
GO; GO:0008166; P:viral replication; TAS.  
DR InterPro; IPR000827; CC chemokine\_fml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.  
FT SIGNAL 1 23  
FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A3.  
FT DISULFID 33 57 BY SIMILARITY.  
FT DISULFID 34 73 BY SIMILARITY.  
FT MUTAGEN 49 49 D->A; IN BB-10010; IMPROVED  
PHARMACEUTICAL PROPERTIES.  
SQ SEQUENCE 92 AA; 10085 MW; 517865D5D6776CA8 CRC64;  
Query Match 61.8%; Score 300.5; DB 1; Length 92;  
Best Local Similarity 57.6%; Pred. No. 1.8e-26;  
Matches 53; Conservative 19; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 MKLCVTVLLMLVAFCSPALSPAGSPPTACCSYTKLPRNFVVDYVETSLCSQ 60  
Db 1 MQVSTAAALVLLCTMALCN-QFSASLAADPTACCSYTSRQIPQFIADYPTSSQCSK 59  
Qy 61 PAVVFOYTKSKQVCADPSWSVOEYVYDLELN 92  
Db 60 PGVIFLTKSRQVCADPSEEWQKYVSDLELS 91  
RESULT 9  
SY04 CHICK STANDARD; PRT; 90 AA.  
AC Q30826; Q910C9;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Small inducible cytokine A4 homolog precursor (Macrophage inflammatory  
protein 1-beta homolog).  
DE protein 1-beta homolog.  
GN CCL4 OR SCY44.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=95369710; PubMed=7642115;  
RA Petrenko O., Ischenko I., Enrietto P.J.;  
RT "Isolation of a cDNA encoding a novel chicken chemokine homologous to  
mammalian macrophage inflammatory protein-1 beta.";  
RL Gene 160:305-306(1995).  
RN (2)  
RP SEQUENCE FROM N.A.  
RA Hughes S.M., Bumstead N.;  
RT "Mapping of the gene encoding the chicken homologue of the mammalian  
chemokine SCY44.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN (3)  
RP SEQUENCE OF 14-90 FROM N.A.  
RA Petrenko O., Enrietto P.J.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES  
(BY SIMILARITY).

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EMBL; AJ007043; CAA07430.1; HSP; P13501; IRTN. InterPro; IPR000827; CC\_chemkine\_sml. InterPro; IPR001811; Chemokine\_IL8. Pfam; PF00048; IL8; 1. SMART; PS00199; SCV; 1. PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1. Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response. SIGNAL 1 23 POTENTIAL. CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5. DISULFID 33 57 BY SIMILARITY. FT DISULFID 34 73 BY SIMILARITY. SQ SEQUENCE 91 AA; 10073 MW; 660DD38E015B0735 CRC64;

Query Match 50.7%; Score 246.5; DB 1; Length 91; Best Local Similarity 48.9%; Pred. No. 1.6e-20; Matches 45; Conservative 20; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKLCVTYLSLMLVAAPCSALPAGMSDPTACCFSTARKLPNRFVVDYVETSLCSQ 60  
Dd 1 MKVSATAFAVLMLAAALCAPASAPYASD-TTCCPAYISRPLRTHVQYFYTSSKCSM 59  
QY 61 PAVVFQTKRSKQVADPSWSWQVYVVDLELN 92  
Dd 60 AAVVFITRKQRCVCAPEKWKVREYNALSL 91

RESULT 11  
SY05\_HUMAN  
ID SY05\_HUMAN STANDARD; PRT; 91 AA.  
AC P13501; OX3646; Q9WY42.  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta) (T cell-specific protein P228) (TCP228).  
GN CCL5 OR SCV45.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88285659; PubMed=2456327;  
RA Schall T.J., Jongstra J., Dyer B.J., Jorgensen J., Clayberger C., Davis M.M., Krensky A.M.;  
RT "A human T cell-specific molecule is a member of a new gene family";  
RL J. Immunol. 141:1018-1025(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Jang J.S., Kim B.E.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99228475; PubMed=10213461;  
RA Nomiya H., Fukuda S., Iio M., Tanase S., Miura R., Yoshie O.;  
RT "Organization of the chemokine gene cluster on human chromosome 17q11.2 containing the genes for CC chemokine MIP-1, HCC-2, LEC, and RANTES";  
RL J. Interferon Cytokine Res. 19:227-234(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Zeng Q.P., Yang R.Y., Fu L.C.;  
RT "The complete sequence of human beta-chemokine RANTES mRNA";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RT TISSUE=Brain;

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EMBL; L34553; AAP48747.1; HSP; P13236; IHUM. InterPro; IPR000827; CC\_chemkine\_sml. InterPro; IPR001811; Chemokine\_IL8. Pfam; PF00048; IL8; 1. SMART; PS00199; SCV; 1. PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1. Cytokine; Chemotaxis; Signal. SIGNAL 1 21 BY SIMILARITY. CHAIN 22 90 SMALL INDUCIBLE CYTOKINE A4 HOMOLOG. DISULFID 32 56 BY SIMILARITY. FT DISULFID 33 72 BY SIMILARITY. T CONFLICT 87 87 M -> L (IN REF. 1). SQ SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;

Query Match 54.3%; Score 264; DB 1; Length 90; Best Local Similarity 51.1%; Pred. No. 1.8e-22; Matches 45; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

Y 5 VTLSLMLVAAPCSALPAGMSDPTACCFSTARKLPNRFVVDYVETSLCSQPAVV 64  
b 3 VSAVALVLLIACYOTSAAPVGSDEPTSCCTYISQQLFFSFADYVETNSQCPHAGV 62  
Y 65 FQTKRSKQVADPSWSWQVYVVDLELN 92  
b 63 FITRKREVCANPENVQDYVWYMKMELN 90

RESULT 10  
SY05\_BOVIN  
ID SY05\_BOVIN STANDARD; PRT; 91 AA.  
AC O97919;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta).  
GN CCL5 OR SCV45.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
RX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RT TISSUE=Intestine;  
RA Aust G., Thamm B., Rost A.K.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).

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EMBL; W21121; AAA36725.1; -;  
EMBL; AF043341; AAC03541.1; -;  
EMBL; AF088219; AAC63331.1; -;  
EMBL; AF266753; AAF73070.1; -;  
EMBL; BC008600; AAHG8600.1; -;  
PIR; A28815; A28815.  
PDB; 1HRJ; 14-OCT-95.  
PDB; 1RTN; 03-JUN-95.  
PDB; 1ETO; 03-JUN-95.  
PDB; 1B3A; 23-APR-99.  
PDB; 1EQT; 19-APR-00.  
Genew; HGNC:10632; CCL5.

GO: 0000380; P:antiviral response protein activity; TAS.  
 GO: 0000380; P:antiviral response protein activity; TAS.  
 GO: 0000809; P:chemokine activation; TAS.  
 GO: 0000874; P:calcium ion homeostasis; TAS.  
 GO: 0000715; P:cell adhesion; TAS.  
 GO: 0006928; P:cell motility; TAS.  
 GO: 0000726; P:cell-cell signaling; TAS.  
 GO: 0000968; P:cellular defense response; TAS.  
 GO: 0006935; P:chemotaxis; TAS.  
 GO: 0006887; P:exocytosis; TAS.  
 GO: 0006954; P:inflammatory response; TAS.  
 GO: 0006979; P:response to oxidative stress; TAS.  
 GO: 0006915; P:response to viruses; TAS.  
 GO: 00007165; P:signal transduction; TAS.  
 InterPrt: IPR000827; CC\_chemokine\_enl.  
 InterPrt: IPR001811; Chemokine IL8.

DR SMART; SM00199; SCY; 1.  
DR PROSTGE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response;  
KW 3D-structure.

[illegible]

```

STRAND 30 33
HELIX 44 46
STRAND 47 52
TURN 55 56
STRAND 62 66
TURN 67 68
STRAND 71 74
TURN 76 77
HELIX 79 91
SO SEQUENCE 91 AA: 9930 MW: FBOBF9A87C620F CRC64:

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Query March	50.5%;	Score 245.5;	DB 1;	Length 91;
Best Local Similarity	45.7%;	Pred. No. 2e-20;		
Matches	42	Conservative	26	Indels
Matches	42	Conservative	26	Indels

[illegible]

RESULT 12		
SY05 MOUSE		
ID _SY05_MOUSE	STANDARD;	PRT; 91 AA.
AC P30882;		
DT 01-JUL-1993	(Rel. 26. Created)	

Downloaded from <http://ajph.org/> on November 10, 2014

MEDLINE=223388257; PubMed=12477932;

Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altshul S.F., Zdobych B., Buetow K.H., Schaefer C.F., Shat N.K., Hotkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Feingold E., Hulton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting J., Helton E., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).

[6]

SEQUENCE OF 49-56; 71-79 AND 83-91, AND FUNCTION.

MEDLINE=96106406; PubMed=85253373;

Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C., Lusso P.;

"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells.";

Science 270:1811-1815(1995).

[7]

STRUCTURE BY NMR.

MEDLINE=9532612; PubMed=7542919;

Chung C.-W., Cooke R.M., Proudfoot A.E.I., Wells T.N.C.;

"The three-dimensional solution structure of RANTES.";

Biochemistry 34:9307-9314(1995).

[8]

STRUCTURE BY NMR.

MEDLINE=95244456; PubMed=7537089;

Skelton N.J., Aspiras F., Ogez J., Schall T.J.;

"Proton NMR assignments and solution conformation of RANTES, a chemokine of the C-C type.";

Biochemistry 34:5329-5342(1995).

[9]

SYNTHESIS, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).

MEDLINE=99111238; PubMed=989151;

Wilken J., Hoover D., Thompson D.A., Barlow P.N., McSparron H., Picard L., Wlodawer A., Lubkowski J., Kent S.B.;

"Total chemical synthesis and high-resolution crystal structure of the potent anti-HIV protein AOP-RANTES.";

Chem. Biol. 6:43-51(1999).

[10]

X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).

Hoover D.M., Shaw J., Gryczynski Z., Proudfoot A.E.I., Wells T.N.C., Lubkowski J.;

"The crystal structure of Met-RANTES: comparison with native RANTES and AOP-RANTES.";

Protein Rept. Lett. 7:73-82(2000).

-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.

-!- INDUCTION: By mitogens

-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).

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01-JUN-1994 (Rel. 29, Last sequence update)  
 15-SEP-2003 (Rel. 42, Last annotation update)  
 Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta) (Murantes).  
 CCL5 OR SCYAs.  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=92277990; PubMed=1375672;  
 Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,  
 Krensky A.M., Neilson E.G.;  
 "Isolation and characterization of cDNA from renal tubular epithelium encoding murine Rantes.";  
 Kidney Int. 41:220-225(1992).  
 [2]  
 SEQUENCE FROM N.A.  
 MEDLINE=92298805; PubMed=1376260;  
 Schall T.J., Simpson N.J., Mac J.Y.;  
 "Molecular cloning and expression of the murine RANTES cytokine: structural and functional conservation between mouse and man.";  
 Eur. J. Immunol. 22:1477-1481(1992).  
 [3]  
 SEQUENCE FROM N.A.  
 STRAIN=NIH Swiss;  
 MEDLINE=94133613; PubMed=7507961;  
 Danoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;  
 "Cloning, genomic organization, and chromosomal localization of the Scy5 gene encoding the murine chemokine RANTES.";  
 J. Immunol. 152:1182-1189(1994).  
 [4]  
 SEQUENCE FROM N.A.  
 STRAIN=BA1B/Cr;  
 MEDLINE=94217689; PubMed=7513046;  
 Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,  
 Paznekas W.A.;  
 "Definition of a lipopolysaccharide-responsive element in the 5'-flanking regions of Murantes and crg-2.";  
 Mol. Cell. Biol. 14:2914-2925(1994).  
 [5]  
 SEQUENCE FROM N.A.  
 STRAIN=B10.S/J, BALB/CJ, DBA/2J, NOD/LTJ, and SJL/J; TISSUE=spleen;  
 MEDLINE=99370037; PubMed=10438970;  
 Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
 Blankenhorn E.P.;  
 "Sequence polymorphisms in the chemokines Scy1 (TCA-3), Scy2 (monocyte chemoattractant protein (MCP)-1), and Scy12 (MCP-5) are candidates for eae7, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";  
 J. Immunol. 163:2262-2266(1999).  
 [6]  
 SEQUENCE FROM N.A.  
 STRAIN=129/Sv;  
 Nomiya H.;  
 "Organization of the mouse CC chemokine cluster containing the genes for C10, MRP-2 and RANTES.";  
 Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 [7]  
 SEQUENCE FROM N.A.  
 STRAIN=C57BL/6J; TISSUE=Pancreas;  
 PubMed=12466851;  
 Okazaki Y., Osato N., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 Nakaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 Konagata A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,  
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
 Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 Hara A., Hashizume W., Imotani K., Isehi Y., Itoh M., Kagawa I.,  
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 Birney E., Hayashizaki Y.;  
 "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 Nature 420:563-573(2002).  
 [8]  
 SEQUENCE FROM N.A.  
 TISSUE=Mammary gland;  
 PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,  
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 -!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS.  
 -!- SUBCELLULAR LOCATION: Secreted.  
 -!- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.  
 -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).  
 -----  
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 -----  
 EMBL; M77747; AAA40029.1; -  
 EMBL; S37648; AAB22330.1; -  
 EMBL; U02298; AAB18302.1; -  
 EMBL; X70675; CAAS0011.1; -  
 EMBL; AF065944; AAC17511.1; -  
 EMBL; AF065945; AAC17512.1; -  
 EMBL; AF065946; AAC17513.1; -  
 EMBL; AF065947; AAC17514.1; -  
 EMBL; AF128187; AAF22528.1; -  
 EMBL; AB051897; BAB18731.1; -  
 EMBL; AK03101; BAB22566.1; -  
 EMBL; BC033508; AAB33508.1; -  
 EMBL; I48875; A46539.  
 HSSP; P13501; 1RTN.

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MGD; MGI:98262; Cells.
InterPro; IPR000827; CC chemokine sm1.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
CHAIN 1 23
SIGNAL 1 23
DISULFID 24 91
DISULFID 33 57
DISULFID 34 73
CONFLICT 19 19
CONFLICT 41 41
SEQUENCE 91 AA; 10071 MW; 5DFD66F4664FE1C8 CRC64;

Query Match 49.9%; Score 242.5; DB 1; Length 91;
Best Local Similarity 48.9%; Pred. No. 4.4e-20;
Matches 45; Conservative 20; Mismatches 26; Indels 1; Gaps 1;

1 MKLCVTVLSLMLVAAPSPALSPMGSDPTACCFSTARKLPNRFVVDYETSSLSQ 60
1 MKISAALTLTILTAALCTPASPYPGSD-TTPCCFAYLSALPRAHVKEYFYTSKCSN 59
61 PAVVFTQKRSKQVACDPSSESWQVEYVYDLEIN 92
60 LAVVFTRRNQVCANPEKKVQVEYINYLEMS 91

RESULT 13
SY05 SIGHI STANDARD; PRT; 91 AA.
09121;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein).
CCL5 OR SCYAS.
Sigmodon hispidus (Hispid cotton rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae; Sigmodon.
NCBI_TaxID=42415;
SEQUENCE FROM N.A.
Blanco J.C., Pletneva L.M., Prince G.A.;
"Sigmodon hispidus cytokines, chemokines and interferons."
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
!- SUBCELLULAR LOCATION: Secreted.
!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).

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EMBL; AF421391; AAL16932.1; -
InterPro; IPR000827; CC chemokine sm1.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
CHAIN 1 23
SIGNAL 1 23
DISULFID 24 91
DISULFID 33 57
CONFLICT 19 19
CONFLICT 41 41
SEQUENCE 91 AA; 10071 MW; 5DFD66F4664FE1C8 CRC64;

Query Match 49.9%; Score 242.5; DB 1; Length 91;
Best Local Similarity 48.9%; Pred. No. 4.4e-20;
Matches 45; Conservative 20; Mismatches 26; Indels 1; Gaps 1;

1 MKLCVTVLSLMLVAAPSPALSPMGSDPTACCFSTARKLPNRFVVDYETSSLSQ 60
1 MKISAALTLTILTAALCTPASPYPGSD-TTPCCFAYLSALPRAHVKEYFYTSKCSN 59
61 PAVVFTQKRSKQVACDPSSESWQVEYVYDLEIN 92
60 LAVVFTRRNQVCANPEKKVQVEYINYLEMS 91

RESULT 14
SY05 CAVPO STANDARD; PRT; 91 AA.
097272; O09076;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIG-delta).
CCL5 OR SCYAS.
Cavia porcellus (Guinea pig).
Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
SEQUENCE FROM N.A.
STRAIN=Dunkin-Hartley;
Campbell E.M., Proudfoot A.E.J., Yoshimura T., Allet B., Wells T.N.C., White A.M., Westwick J., Watson M.L.;
Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
TISSUE=Lung;
Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A., Yamaguchi K., Kanazawa M.;
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
!- SUBCELLULAR LOCATION: Secreted.
!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).

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EMBL; U77037; AAC53293.1; -
EMBL; AB026622; BAA19604.1; -
HSP; P13501; IRTN.
InterPro; IPR000827; CC chemokine sm1.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
CHAIN 1 23
SIGNAL 1 23
DISULFID 24 91
DISULFID 33 57
BY SIMILARITY.
FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
FT DISULFID 33 57 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
SEQUENCE 91 AA; 10088 MW; 7F6A31B751337DB9 CRC64;

Query Match 48.3%; Score 234.5; DB 1; Length 91;

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Search completed: December 16, 2003, 15:38:21  
Job time : 10.5574 secs

Best Local Similarity 45.7%, Pred. No. 3.3e-19;  
Matches 42; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

1 MKLCVTVLMLVAALFCSFALSPAGSDPPTACCFSTYARKLPNFWVDYVYETSSLCQ 60  
1 MKVSAALCVLITLALCVASASPYASD-TTPCCFAYISRALPRTHIKEYFYVTSKCSN 59  
61 PAVVFTQKRSKQVADPSESWSQVYVVDLELN 92  
60 LAVVFTVRNQRVCANPEKKWVREYINSLEMS 91

RESULT 15

705\_RAT STANDARD: PRT: 92 AA.  
SY05\_RAT  
P50231;  
01-OCT-1996 (Rel. 34, Created)  
01-OCT-1996 (Rel. 34, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta).  
CCL5 OR SCYAS.  
Rattus norvegicus (Rat).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
[1]\_  
SEQUENCE FROM N.A. TISSUE=Lung;  
STRAIN=Long Evans;  
Jones M.L., Shanley T.P., Ward P.A.;  
Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER  
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).  
SUBCELLULAR LOCATION: Secreted.  
SIMILARITY: BELONGS TO THE INTERCINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC).  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
EMBL; U06436; AAA96499.1; -  
HSP; P13501; 1RTN.  
InterPro; IPR000827; CC\_chemokine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
SIGNAL 1 24 POTENTIAL.  
CHAIN 25 92 SMALL INDUCIBLE CYTOKINE A5.  
DISULFID 34 58 BY SIMILARITY.  
DISULFID 35 74 BY SIMILARITY.  
SEQUENCE 92 AA; 10170 MW; B4FBC2B4208ABC6 CRC64;..

Query Match 47.1%, Score 229; DB 1; Length 92;  
Best Local Similarity 47.3%, Pred. No. 1.4e-18;  
Matches 44; Conservative 21; Mismatches 26; Indels 2; Gaps 2;

1 MKLCVTV-LSLMLVAALFCSFALSPAGSDPPTACCFSTYARKLPNFWVDYVYETSSLCQ 59  
1 MKISAASLVILVAALCTFVPASPYGSD-TTPCCFAYLSLALPRAHVKEYFYVTSKCS 59  
60 QPAVFTQKRSKQVADPSESWSQVYVVDLELN 92  
60 NLAVVFTVRNQRVCANPEKKWVREYINSLEMS 92

GenCore version 5.1.6  
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protein - protein search, using sw model

n on: December 16, 2003, 15:36:20 ; Search time 30.6667 Seconds  
(without alignments)  
774.158 Million cell updates/sec

US-09-920-137a-7

effect score: 486  
quence: 1 MKLCVTVLSLLMLVAAPFCSP.....VCADPSESWMQYVYDLELN 92

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 830525 seqs, 258052604 residues

tal number of hits satisfying chosen parameters: 830525

nimum DB seq length: 0  
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

tabase :

- 1: sp archaea:\*
- 2: sp bacteria:\*
- 3: sp fungi:\*
- 4: sp human:\*
- 5: sp invertebrate:\*
- 6: sp mammal:\*
- 7: sp mhc:\*
- 8: sp organelle:\*
- 9: sp phage:\*
- 10: sp plant:\*
- 11: sp rodent:\*
- 12: sp virus:\*
- 13: sp vertebrate:\*
- 14: sp unclassified:\*
- 15: sp xvirus:\*
- 16: sp bacteriap:\*
- 17: sp archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	468	96.3	92	Q8NHW4	Q8NHW4 homo sapien
2	459	94.4	92	Q8HYQ2	Q8HYQ2 macaca mula
3	376	77.4	92	Q91ZL0	Q91ZL0 sigmodon hi
4	320	65.8	93	Q8SOA6	Q8SQa6 bos taurus
5	294.5	60.6	92	Q91Z65	Q91Z65 sigmodon hi
6	281.5	57.9	92	Q8HYQ3	Q8HYQ3 macaca mula
7	271.5	55.9	80	Q14745	Q14745 homo sapien
8	264	54.3	90	Q9PWa6	Q9PWa6 gallus gall
9	252	51.9	49	Q8HYN3	Q8HYN3 macaca mula
10	249	51.2	56	Q8HYN4	Q8HYN4 macaca mula
11	245.5	50.5	89	Q91820	Q91820 gallus gall
12	243.5	50.1	91	Q8MKD0	Q8MKD0 equus cabal
13	240.5	49.5	91	Q8HYQ1	Q8HYQ1 macaca mula
14	233.5	48.0	91	Q8QGS7	Q8QGS7 gallus gall
15	225.5	46.4	91	Q8HYS0	Q8HYS0 canis famul
16	224	46.1	92	Q8SQ40	Q8SQ40 felis silve

17	204	42.0	88	6	Q8HYP8	Q8HYP8 macaca mula
18	189.5	39.0	91	13	Q8QGS6	Q8QGS6 gallus gall
19	184.5	38.0	148	11	Q9QYD7	Q9QYD7 mus musculu
20	182	37.4	150	11	Q8CGM5	Q8CGM5 sigmodon hi
21	179.5	36.9	99	6	Q9TTQ3	Q9TTQ3 equus cabal
22	179.5	36.9	100	6	Q9TTQ4	Q9TTQ4 equus cabal
23	178	36.6	92	6	Q8MI76	Q8MI76 bos taurus
24	174.5	35.9	99	6	Q8MKC8	Q8MKC8 equus cabal
25	170.5	35.1	97	6	Q8MIT7	Q8MIT7 macaca mula
26	168.5	34.7	99	6	Q8HYQ0	Q8HYQ0 macaca mula
27	166.5	34.3	100	6	Q9SMD5	Q9SMD5 bos taurus
28	165.5	34.1	97	6	Q8HXZ5	Q8HXZ5 macaca mula
29	164	33.7	50	6	Q8HYN5	Q8HYN5 macaca mula
30	162.5	33.4	81	6	Q9TTQ2	Q9TTQ2 equus cabal
31	160	32.9	97	6	Q9TT86	Q9TT86 bos taurus
32	157.5	32.4	95	12	Q98158	Q98158 kaposi's sa
33	157.5	32.4	119	11	Q8K477	Q8K477 rattus norv
34	153	31.5	75	6	Q9TTQ1	Q9TTQ1 equus cabal
35	150.5	31.0	91	13	Q8JIM5	Q8JIM5 paralicthy
36	150.5	31.0	91	13	Q8AV56	Q8AV56 paralicthy
37	149.5	30.8	91	13	Q8JIM4	Q8JIM4 paralicthy
38	145	29.8	131	6	Q8HYP5	Q8HYP5 macaca mula
39	137.5	28.3	92	11	Q9QZU2	Q9QZU2 mus musculu
40	137.5	28.3	92	11	Q91ZHS	Q91ZHS rattus norv
41	136.5	28.1	101	12	Q8JRS7	Q8JRS7 guinea pig
42	136	28.0	120	6	Q8HYP4	Q8HYP4 macaca mula
43	135.5	27.9	81	11	Q9QZU1	Q9QZU1 rattus norv
44	135	27.8	95	13	Q8AYB2	Q8AYB2 ictalurus p
45	133.5	27.5	97	11	Q9Z318	Q9Z318 cavia porce

ALIGNMENTS

RESULT 1

Q8NHW4 ID Q8NHW4 PRELIMINARY; PRT; 92 AA.  
AC Q8NHW4;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Macrophage inflammatory protein-1b2.  
GN CCL4L1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nibbs R.J., Barcellos L.F., Townson J.R.;  
RT "Variation in gene copy number of the human chemokines macrophage  
inflammatory protein-1a/CCL3 and macrophage inflammatory protein-  
1b/CCL4";  
RT 1b/CCL4";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY079147; AL87008.1;  
DR InterPro: IPR000827; CC chemokine sml.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00472; SMALL\_CYTOKINES CC; 1.  
SQ SEQUENCE 92 AA; 10166 MW; 4C8D01E926CDE882 CRC64;

Query Match 96.3%; Score 468; DB 4; Length 92;  
Best Local Similarity 96.7%; Pred. No. 1.8e-49;  
Matches 89; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLCVTVLSLLMLVAAPFCSPALAPMGSDPPTACCFSTYARKLPKRNFRVVDYVYETSLCSQ 60

Db 1 MKLCVTVLSLLMLVAAPFCSPALAPMGSDPPTACCFSTYARKLPKRNFRVVDYVYETSLCSQ 60

Qy 61 PAVVFQTKRSKQVCADPSESWMQYVYDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESWMQYVYDLELN 92





[illegible]

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OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hofmann-Lehmann R., Williams A.L., Swenerton R.K., Li P.-L.,
RT Rasmussen R.A., Chenine A.-L., McClure H.M., Ruprecht R.M.;
RT "Quantification of Simian Cytokine and Beta-Chemokine mRNAs using
RT Real-Time Reverse-Transcriptase Polymerase Chain Reaction: Variations
RT in Expression during Chronic Primate Lentivirus Infection.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF457196; AAN76986.1; -.
DR NON_TER 1
FT NON_TER 49
FT NON_TER 1
SQ SEQUENCE 49 AA; 5663 MW; D205B56BF349A6CA CRC64;

Query Match 51.9%; Score 252; DB 6; Length 49;
Best Local Similarity 93.9%; Pred. No. 2.2e-23;
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 35 CFSYTARKLPNFVVDVYETSSLCSPAVVFTQKRSQVCAADPSESQVQ 83
Db 1 CFSYTVRKLPNFVVDVYETSSLCSPAVVFTQKRGQVCAADPSETWVQ 49

RESULT 10
Q8HYN4
ID Q8HYN4 PRELIMINARY; PRT; 56 AA.
AC Q8HYN4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Macrophage inflammatory protein 1 alpha (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hofmann-Lehmann R., Williams A.L., Swenerton R.K., Li P.-L.,
RT Rasmussen R.A., Chenine A.-L., McClure H.M., Ruprecht R.M.;
RT "Quantification of Simian Cytokine and Beta-Chemokine mRNAs using
RT Real-Time Reverse-Transcriptase Polymerase Chain Reaction: Variations
RT in Expression during Chronic Primate Lentivirus Infection.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF457195; AAN76985.1; -.
DR NON_TER 1
FT NON_TER 56
FT NON_TER 56
SQ SEQUENCE 56 AA; 6442 MW; EB12A0E0D41D6F68 CRC64;

Query Match 51.2%; Score 249; DB 6; Length 56;
Best Local Similarity 73.2%; Pred. No. 6e-23;
Matches 41; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 31 PTACCSYFARKLPNFVVDVYETSSLCSPAVVFTQKRSQVCAADPSESQVQ 86
Db 1 PTACCSYFARKLPNFVVDVYETSSLCSPAVVFTQKRSQVCAADPSESQVQ 56

RESULT 11
Q918E0
ID Q918E0 PRELIMINARY; PRT; 89 AA.
AC Q918E0
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Chemokine K203 precursor.
GN K203.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RA Sick C., Schneider K., Staeheli P., Weining K.C.;
RT "Novel chicken CXCR and CC chemokines.";
RL Cytokine 12:181-186(2000).
DR EMBL; Y18692; CAB70956.1; -.
DR HSSP; P13236; LHUM.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 89
FT CHAIN 22 89
SQ SEQUENCE 89 AA; 9896 MW; 6FA2EA7A4950CA75 CRC64;

Query Match 50.5%; Score 245.5; DB 13; Length 89;
Best Local Similarity 50.0%; Pred. No. 2.6e-22;
Matches 45; Conservative 20; Mismatches 22; Indels 3; Gaps 2;

QY 1 MKLCVTVLISLLMLVAAPCSFALSPMGSDPPTACCFSTARKLPNFVVDVYETSSLCQ 60
Db 1 MKLSAVLAL--LIASFCSRASSAPVGDVPT-CCTTITHKIPRNLIQRHYSTISCSK 57

QY 61 PAVVFQTKRSQVCAADPSESQVQVYVDLE 90
Db 58 PAIIFITKREVCANPSDPVQVYLQSVK 87

RESULT 12
Q8MKD0
ID Q8MKD0 PRELIMINARY; PRT; 91 AA.
AC Q8MKD0
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Small inducible cytokine A5 RANTES.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RT "Equus caballus RANTES mRNA.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506970; AAM34212.1; -.
DR InterPro; IPR000827; CC chemokine sm1.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 91 AA; 10159 MW; ABB253E8CD4ED7FD CRC64;

Query Match 50.1%; Score 243.5; DB 6; Length 91;
Best Local Similarity 46.7%; Pred. No. 4.7e-22;
Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKLCVTVLISLLMLVAAPCSFALSPMGSDPPTACCFSTARKLPNFVVDVYETSSLCQ 60
Db 1 MKVFAALAVILATATCTFASAPYASD-TTPCCPAYISRPLPRAHIQIEYFTSSKCSI 59

QY 61 PAVVFQTKRSQVCAADPSESQVQVYVDLEIN 92
Db 60 PAVVFQTKRSQVCAADPSESQVQVYVDLEIN 91

RESULT 13
Q8HYQ1
ID Q8HYQ1 PRELIMINARY; PRT; 91 AA.
AC Q8HYQ1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chemokine CCL5/RANTES.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Comprehensive cloning and sequencing reveals evolutionary
RT conservation among all groups of rhesus macaque chemokines."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF449268; AAN76072.1; -
DR EMBL; AF449268; AAN76072.1; -
SQ SEQUENCE 91 AA; 10019 MW; BCBDE69ED0573803B CRC64;

Query Match 49.5%; Score 240.5; DB 6; Length 91;
Best Local Similarity 45.7%; Pred. No. 11e-21;
Matches 42; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKLCVTVLSLLMLVAACFSPALSPMGSDPPTACCFSTARKLPNRFVVDYVYETSSLCQ 60
Db 1 MKVSAARLAVILVATLALCAPASPHASD-TTPCCPAYIARPLRAHIKEYEFTSGKCSN 59
QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
Db 60 PAVVFVTRKRVQVCANPEKKVREYINSLEMS 91

RESULT 14
Q8Q57 PRELIMINARY; PRT; 91 AA.
ID Q8Q57;
AC Q8Q57;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Chemokine ah294.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21655115; PubMed=11797102;
RA Hughes S., Haynes A., O'Regan M., Bumstead N.;
RT "Identification, mapping, and phylogenetic analysis of three novel
RT chicken CC chemokines."
RL Immunogenetics 53:674-683 (2001).
DR EMBL; AY037859; AAK84432.1; -
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 91 AA; 10154 MW; 744A64BB229194EF CRC64;

Query Match 48.0%; Score 233.5; DB 13; Length 91;
Best Local Similarity 51.6%; Pred. No. 7.8e-21;
Matches 47; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

QY 1 MKLCVTVLSLLMLVAACFSPALSPMGSDPPTACCFSTARKLPNRFVVDYVYETSSLCQ 60
Db 1 MMTAVAVSLSLILLVAALFPQASSGPFAGD-TTVCCFNYSVKLPQNHVVDYFTSSKCPQ 59
QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 91
Db 60 AAVVFITRKRVQVCANPDARVWVEYINFL 90

RESULT 15
Q8H50 PRELIMINARY; PRT; 91 AA.
ID Q8H50

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AC Q8H50;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RANTES protein.
GN RANTES.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Enomoto A., Kano R., Hasegawa A.;
RT "Molecular cloning of canine RANTES gene."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB098582; BAC53725.1; -
DR EMBL; AB098582; BAC53725.1; -
SQ SEQUENCE 91 AA; 10179 MW; 01D79538CB8148E7 CRC64;

Query Match 46.4%; Score 225.5; DB 6; Length 91;
Best Local Similarity 44.6%; Pred. No. 7.4e-20;
Matches 41; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

QY 1 MKLCVTVLSLLMLVAACFSPALSPMGSDPPTACCFSTARKLPNRFVVDYVYETSSLCQ 60
Db 1 MKVSAATFAILLATATFRAPASPYASD-TTPCCPAYISGRLEPFTHVQEVYFTSSKCSM 59
QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
Db 60 PAVVFVTRKRVQVCANPEKKVREYINSLEMS 91

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Search completed: December 16, 2003, 15:39:36  
Job time : 31.6667 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2003, 15:37:55 ; Search time 167.41 Seconds  
(without alignments)  
500.045 Million cell updates/sec

Title: US-09-920-137A-7

Perfect score: 486

Sequence: 1 MKLCVTVLSLLMLVAFCSP.....VCADPSESWSQYVVDLELN 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Seatched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pending Patents\_AA\_Main:\*

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2:	/cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
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32:	/cgn2_6/ptodata/1/paa/US08 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	486	100.0	92	1 PCT-US94-08207A-28

Sequence 28, Appl

2	486	100.0	92	1 PCT-US94-08207A-28
3	486	100.0	92	1 PCT-US97-17900-10
4	486	100.0	92	1 PCT-US98-04002-10
5	486	100.0	92	5 US-08-136-117-28
6	486	100.0	92	7 US-08-390-740B-7
7	486	100.0	92	8 US-08-467-123-4
8	486	100.0	92	13 US-08-927-939-20
9	486	100.0	92	13 US-08-927-939A-20
10	486	100.0	92	13 US-08-940-687-10
11	486	100.0	92	14 US-09-023-092-8
12	486	100.0	92	14 US-09-081-230-3
13	486	100.0	92	15 US-09-113-705-4
14	486	100.0	92	15 US-09-113-705-7
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16	486	100.0	92	16 US-09-208-803-11
17	486	100.0	92	17 US-09-360-290-7
18	486	100.0	92	17 US-09-387-620-4
19	486	100.0	92	18 US-09-467-638-10
20	486	100.0	92	19 US-09-545-894-10
21	486	100.0	92	22 US-09-791-537-22748
22	486	100.0	92	23 US-09-834-366-17997
23	486	100.0	92	23 US-09-834-794A-31
24	486	100.0	92	23 US-09-834-795A-31
25	486	100.0	92	24 US-09-920-137A-7
26	486	100.0	92	26 US-10-057-275-7
27	486	100.0	92	27 US-10-137-655-7
28	486	100.0	92	27 US-10-158-366-4
29	486	100.0	92	28 US-10-293-705-11
30	486	100.0	92	29 US-10-325-899-9374
31	486	100.0	92	30 US-10-405-027-4023
32	486	100.0	92	32 US-60-197-873-17997
33	486	100.0	92	32 US-60-453-050-9427
34	486	100.0	92	32 US-60-453-135-9427
35	486	100.0	92	32 US-60-455-444-5106
36	486	100.0	92	32 US-60-466-412-9427
37	486	100.0	92	32 US-60-466-412-9427
38	486	100.0	92	32 US-60-474-850-516
39	486	100.0	331	1 PCT-US98-04002-7
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44	482	99.2	92	21 US-09-724-676-63101
45	482	99.2	92	21 US-09-724-676-63102

#### ALIGNMENTS

RESULT 1  
PCT-US94-08207A-28

; Sequence 28, Application PC/TUS9408207A

; GENERAL INFORMATION:

; APPLICANT: The Upjohn Company

; APPLICANT: FOR U.S. PURPOSES ONLY: Hoogewerf, Arlene J. and Ledbetter, Steven R.

; TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND

; TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Upjohn Company, Intellectual Property Law

; STREET: 301 Henrietta

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT-US94/08207A

; FILING DATE:

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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jameson, William G.
; REGISTRATION NUMBER: 27,199
; REFERENCE/DOCKET NUMBER: 4731.1 CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/385-7561
; TELEFAX: 616/385-6897
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-08207A-28

Query Match 100.0%; Score 486; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPALAPMGSDPPTACCFSYTARKLPNPFVVDYVYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAAFCSPALAPMGSDPPTACCFSYTARKLPNPFVVDYVYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92

RESULT 2
PCT-US94-08207-28
; Sequence 28, Application PC/TUS9408207
; GENERAL INFORMATION:
; APPLICANT: Hoogewerf, Arlene J.
; APPLICANT: Ledbetter, Steven R.
; TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND
; TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Upjohn Company, Intellectual Property Law
; STREET: 301 Henrietta
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08207
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jameson, William G.
; REGISTRATION NUMBER: 27,199
; REFERENCE/DOCKET NUMBER: 4731.1 CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/385-7561
; TELEFAX: 616/385-6897
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-08207-28

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; Query Match 100.0%; Score 486; DB 1; Length 92;
; Best Local Similarity 100.0%; Pred. No. 5.1e-48;
; Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPALAPMGSDPPTACCFSYTARKLPNPFVVDYVYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAAFCSPALAPMGSDPPTACCFSYTARKLPNPFVVDYVYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92

RESULT 3
PCT-US97-17900-10
; Sequence 10, Application PC/TUS9717900
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: MCP-4 AND MCP-5: NOVEL CHEMOKINES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/17900
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,128
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 00786/293WO2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US97-17900-10

Query Match 100.0%; Score 486; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPALAPMGSDPPTACCFSYTARKLPNPFVVDYVYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAAFCSPALAPMGSDPPTACCFSYTARKLPNPFVVDYVYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESVMQVEYVVDLELN 92

RESULT 4
PCT-US98-04002-10
; Sequence 10, Application PC/TUS9804002
; GENERAL INFORMATION:

```

APPLICANT: Herrmann, Steve  
ATTORNEY/AGENT INFORMATION:  
NAME: Swenberg, Stephen  
TITLE OF INVENTION: CHEMERIC POLYPEPTIDES CONTAINING  
TITLE OF INVENTION: CHEMERIC POLYPEPTIDES CONTAINING  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/04002  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne  
REGISTRATION NUMBER: P-41,323  
REFERENCE/DOCKET NUMBER: GI5291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US98-04002-10

Query Match 100.0%; Score 486; DB 1; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFALSPMGSDPTACCFSTYARKLPNRFVVDYVYETSSLCSSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSFALSPMGSDPTACCFSTYARKLPNRFVVDYVYETSSLCSSQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92

RESULT 5  
US-08-136-117-28  
Sequence 28, Application US/08136117  
GENERAL INFORMATION:  
APPLICANT: Hoogewerf, Arlene J.  
ATTORNEY/AGENT INFORMATION:  
NAME: Ledbetter, Steven R.  
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Upjohn Company, Intellectual Property Law  
STREET: 301 Henrietta  
CITY: Kalamazoo  
STATE: MI  
COUNTRY: USA  
ZIP: 49001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/136,117

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Jameson, William G.  
REGISTRATION NUMBER: 27,199  
REFERENCE/DOCKET NUMBER: 4731.1 CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 616/385-7561  
TELEFAX: 616/385-6897  
TELEX: 224401  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-136-117-28

Query Match 100.0%; Score 486; DB 5; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFALSPMGSDPTACCFSTYARKLPNRFVVDYVYETSSLCSSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSFALSPMGSDPTACCFSTYARKLPNRFVVDYVYETSSLCSSQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92

RESULT 6  
US-08-390-740B-7  
Sequence 7, Application US/08390740B  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,740B  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: MIP-1b

US-08-390-740B-7

Query Match 100.0%; Score 486; DB 7; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLSQ 60  
Qy 61 PAVVFQTKRSKQVCADPSESWSWQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSWQYVYDLELN 92

## RESULT 7

US-08-467-123-4  
; Sequence 4, Application US/08467123  
; GENERAL INFORMATION:  
; APPLICANT: Coleman, Roger  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
; TITLE OF INVENTION: ITS PRODUCTION AND USES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,123  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/375,346  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0026 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 855-0572  
TELEX:

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-467-123-4

Query Match 100.0%; Score 486; DB 8; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLSQ 60

Qy 61 PAVVFQTKRSKQVCADPSESWSWQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSWQYVYDLELN 92

## RESULT 8

US-08-927-939-20  
; Sequence 20, Application US/08927939  
; GENERAL INFORMATION:  
; APPLICANT: Grainger, David J.  
; APPLICANT: Tatalick, Lauren Marie  
; TITLE OF INVENTION: Compounds and methods to inhibit or  
; TITLE OF INVENTION: augment an inflammatory response.  
; FILE REFERENCE: 295.022US1  
; CURRENT APPLICATION NUMBER: US/08/927,939  
; CURRENT FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-927-939-20

Query Match 100.0%; Score 486; DB 13; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLSQ 60  
Qy 61 PAVVFQTKRSKQVCADPSESWSWQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSWQYVYDLELN 92

## RESULT 9

US-08-927-939A-20  
; Sequence 20, Application US/08927939A  
; GENERAL INFORMATION:  
; APPLICANT: Grainger, David J.  
; APPLICANT: Tatalick, Lauren Marie  
; TITLE OF INVENTION: Compounds and methods to inhibit or  
; TITLE OF INVENTION: augment an inflammatory response.  
; FILE REFERENCE: 1543.001US1  
; CURRENT APPLICATION NUMBER: US/08/927,939A  
; CURRENT FILING DATE: 1997-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-927-939A-20

Query Match 100.0%; Score 486; DB 13; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLSQ 60  
Qy 61 PAVVFQTKRSKQVCADPSESWSWQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSWQYVYDLELN 92

## RESULT 10

US-08-940-687-10  
; Sequence 10, Application US/08940687  
; GENERAL INFORMATION:



```

; APPLICANT: Luster, Andrew D.
; APPLICANT: Garcia-Zepeda, Eduardo A.
; APPLICANT: Saraf, Mandy N.
; TITLE OF INVENTION: MCP-4 AND MCP-5: NOVEL CHEMOKINES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,687
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,128
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 00786/293002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-940-687-10
;
Query Match 100.0%; Score 486; DB 13; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLCVTVLSLLMLVAARCSALAPMGSDPTACCSYTKLPKPRNFVVDYVYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAARCSALAPMGSDPTACCSYTKLPKPRNFVVDYVYETSSLC SQ 60
Qy 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 11
US-09-023-092-8
; Sequence 8, Application US/09023092
; GENERAL INFORMATION:
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Wang, Luquan
; APPLICANT: Zlotnik, Albert
; APPLICANT: Murgolo, Nicholas J.
; APPLICANT: Greene, Jonathan R.
; TITLE OF INVENTION: Mammalian Chemokines; Related Reagents
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,092
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0780
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-023-092-8
;
Query Match 100.0%; Score 486; DB 14; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLCVTVLSLLMLVAARCSALAPMGSDPTACCSYTKLPKPRNFVVDYVYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAARCSALAPMGSDPTACCSYTKLPKPRNFVVDYVYETSSLC SQ 60
Qy 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 12
US-09-081-230-3
; Sequence 3, Application US/09081230
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul
; TITLE OF INVENTION: HUMAN CHEMOKINE ZCHEMO-8
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,230
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

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/ LENGTH: 92 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-091-230-3

Query Match 100.0%; Score 486; DB 14; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFALSPALSGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60
Db 1 MKLCVTVLSLLMLVAAFCSFALSPALSGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60
QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92

RESULT 13
US-09-113-705-4
; Sequence 4, Application US/09113705
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, OLGA
; APPLICANT: COLEMAN, ROGER
; APPLICANT: STUART, SUSAN G.
; TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,705
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/421,144
; FILING DATE: 13-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PP-0031 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-113-705-4

Query Match 100.0%; Score 486; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFALSPALSGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60
Db 1 MKLCVTVLSLLMLVAAFCSFALSPALSGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60
QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
```

```
Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92

RESULT 14
US-09-113-705-7
; Sequence 7, Application US/09113705A
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, OLGA
; APPLICANT: COLEMAN, ROGER
; APPLICANT: STUART, SUSAN G.
; TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
; FILE REFERENCE: PP-0031-1 DIV
; CURRENT APPLICATION NUMBER: US/09/113,705A
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MIP-1b
US-09-113-705-7

Query Match 100.0%; Score 486; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFALSPALSGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60
Db 1 MKLCVTVLSLLMLVAAFCSFALSPALSGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60
QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92

RESULT 15
US-09-150-813-20
; Sequence 20, Application US/09150813
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauren Marie
; APPLICANT: Kanaly, Suzanne T.
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295.027US1
; CURRENT APPLICATION NUMBER: US/09/150,813
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: US 08/927939
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-150-813-20

Query Match 100.0%; Score 486; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFALSPALSGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60
Db 1 MKLCVTVLSLLMLVAAFCSFALSPALSGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60
QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
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Search completed: December 16, 2003, 15:46:43  
Job time : 168.41 secs



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; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1677

Query Match      100.0%; Score 486; DB 7; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFSPALSGSDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60
DB 1 MKLCVTVLSLLMLVAAFCSFSPALSGSDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCAADPSESWMQYVYDLELN 92
DB 61 PAVVFQTKRSKQVCAADPSESWMQYVYDLELN 92

RESULT 3
US-60-485-450-1051
; Sequence 1051, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1051
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1051

Query Match      100.0%; Score 486; DB 7; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFSPALSGSDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60
DB 1 MKLCVTVLSLLMLVAAFCSFSPALSGSDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCAADPSESWMQYVYDLELN 92
DB 61 PAVVFQTKRSKQVCAADPSESWMQYVYDLELN 92

RESULT 4
US-60-485-450-1057
; Sequence 1057, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1057
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1057

Query Match      100.0%; Score 486; DB 7; Length 92;

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Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSFSPALSGSDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60
DB 1 MKLCVTVLSLLMLVAAFCSFSPALSGSDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCAADPSESWMQYVYDLELN 92
DB 61 PAVVFQTKRSKQVCAADPSESWMQYVYDLELN 92

RESULT 5
US-10-332-038A-9
; Sequence 9, Application US/10332038A
; GENERAL INFORMATION:
; APPLICANT: Gryphon Therapeutics, Inc.
; APPLICANT: Offord, Robin
; APPLICANT: Gaertner, Hubert
; APPLICANT: Hartley, Oliver
; TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
; FILE REFERENCE: 03504.271
; CURRENT APPLICATION NUMBER: US/10/332,038A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US 60/217,683
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-038A-9

Query Match      77.2%; Score 375; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 APMGSDPPTACCFSTARKLPNRFVVDYETSSLCSPAVVFTKRSKQVCAADPSESWMQ 83
DB 1 APMGSDPPTACCFSTARKLPNRFVVDYETSSLCSPAVVFTKRSKQVCAADPSESWMQ 60

QY 84 EYVYDLELN 92
DB 61 EYVYDLELN 69

RESULT 6
US-10-622-134-10
; Sequence 10, Application US/10622134
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/622,134
; FILING DATE: 18-Jul-2003
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,038
; FILING DATE: 14-Apr-1999
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9319984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-622-134-10

Query Match 76.3%; Score 371; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 8.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PMGSDPTACFSYTKARKLPNRFVVDYETSSLSQSPAVVFTQKRSKQVCADPSESWMQ 84
DB 1 PMGSDPTACFSYTKARKLPNRFVVDYETSSLSQSPAVVFTQKRSKQVCADPSESWMQ 60
QY 85 YVYDLELN 92
DB 61 YVYDLELN 68

RESULT 7
US-60-487-610-1667
; Sequence 1667, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; NUMBER OF SEQ ID NOS: 97101
; CURRENT FILING DATE: 2003-07-17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1667
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1667

Query Match 73.9%; Score 359; DB 7; Length 72;
Best Local Similarity 78.3%; Pred. No. 2.4e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPTACFSYTKARKLPNRFVVDYETSSLSQ 60
DB 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPTACFSYTKARKLPNRFVVDYETSSLSQ 60
QY 61 PAVVFTQKRSKQVCADPSESWMQYVYDLELN 92
DB 61 PAV-----EYVYDLELN 72

RESULT 8
US-60-485-450-1052
; Sequence 1052, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1052
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1052

Query Match 73.9%; Score 359; DB 7; Length 72;
Best Local Similarity 78.3%; Pred. No. 2.4e-35;
Matches 72; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPTACFSYTKARKLPNRFVVDYETSSLSQ 60
DB 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPTACFSYTKARKLPNRFVVDYETSSLSQ 60
QY 61 PAVVFTQKRSKQVCADPSESWMQYVYDLELN 92
DB 61 PAV-----EYVYDLELN 72

RESULT 9
US-10-398-457-5
; Sequence 5, Application US/10398457
; GENERAL INFORMATION:
; APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
; TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
; FILE REFERENCE: WO465
; CURRENT APPLICATION NUMBER: US/10/398,457
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Escherichia Coli
US-10-398-457-5

Query Match 73.5%; Score 357; DB 6; Length 69;
Best Local Similarity 95.7%; Pred. No. 4e-35;
Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 24 APMGSDPTACFSYTKARKLPNRFVVDYETSSLSQSPAVVFTQKRSKQVCADPSESWMQ 83
DB 1 APMGSDPTACFSYTKARKLPNRFVVDYETSSLSQSPAVVFTQKRSKQVCADPSESWMQ 60
QY 84 EYVYDLELN 92
DB 61 EYVYDLELN 69

RESULT 10
PCT-US03-21703-42
; Sequence 42, Application PC/TUS0321703
; GENERAL INFORMATION:
; APPLICANT: Rupp, Fabio
; APPLICANT: Wang, Jianrui
; APPLICANT: Zhou, Ping
; APPLICANT: Wehrman, Tom

```

; APPLICANT: Wang, Zhiwei  
 ; APPLICANT: Tang, Y. Iom  
 ; TITLE OF INVENTION: Methods and Materials Relating to Novel Polypeptides and Polynucleotides  
 ; FILE REFERENCE: HYS-B2 PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US03/21703  
 ; PRIOR FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: PCT/US02/29636  
 ; PRIOR FILING DATE: 2002-09-18  
 ; PRIOR APPLICATION NUMBER: 60/395,402  
 ; PRIOR FILING DATE: 2002-07-12  
 ; PRIOR APPLICATION NUMBER: PCT/US02/22858  
 ; PRIOR FILING DATE: 2002-07-19  
 ; PRIOR APPLICATION NUMBER: 10/112,944  
 ; PRIOR FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: 60/306,971  
 ; PRIOR FILING DATE: 2001-07-21  
 ; PRIOR APPLICATION NUMBER: 10/296,115  
 ; PRIOR FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 09/488,725  
 ; PRIOR FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: 60/418,132  
 ; PRIOR FILING DATE: 2002-10-11  
 ; PRIOR APPLICATION NUMBER: PCT/US02/39555  
 ; PRIOR FILING DATE: 2002-12-10  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 110  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 42  
 ; LENGTH: 92  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 PCT-US03-21703-42

Query Match 61.8%; Score 300.5; DB 1; Length 92;  
 Best Local Similarity 57.6%; Pred. No. 2.6e-28;  
 Matches 53; Conservative 19; Mismatches 19; Indels 1; Gaps 1;  
 QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNFVVDYETSSLSQ 60  
 DB 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPTACCFSTSRQIPQNFADYFETSSQCSK 59  
 QY 61 PAVVFTKRSKQVCAADPSEWQYVYDLELN 92  
 DB 60 PGVIFLTRKGRQVCAADPSEWQYVYDLELN 91

RESULT 11  
 US-60-487-610-1678  
 ; Sequence 1678, Application US/60487610  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: HUANG, Hongjin  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
 ; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001469  
 ; CURRENT APPLICATION NUMBER: US/60/487,610  
 ; CURRENT FILING DATE: 2003-07-17  
 ; NUMBER OF SEQ ID NOS: 97101  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1678  
 ; LENGTH: 92  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-487-610-1678

Query Match 61.0%; Score 296.5; DB 7; Length 92;  
 Best Local Similarity 56.5%; Pred. No. 7.8e-28;  
 Matches 52; Conservative 19; Mismatches 20; Indels 1; Gaps 1;  
 QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNFVVDYETSSLSQ 60

Db 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPTACCFSTSRQIPQNFADYFETSSQCSK 59  
 QY 61 PAVVFTKRSKQVCAADPSEWQYVYDLELN 92  
 Db 60 PGVIFLTRKGRQVCAADPSEWQYVYDLELN 91  
 RESULT 12  
 US-60-485-450-1058  
 ; Sequence 1058, Application US/60485450  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele  
 ; APPLICANT: CHANG, Sheng-Yung  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
 ; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001470  
 ; CURRENT APPLICATION NUMBER: US/60/485,450  
 ; CURRENT FILING DATE: 2003-07-09  
 ; NUMBER OF SEQ ID NOS: 47859  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1058  
 ; LENGTH: 92  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-485-450-1058

Query Match 61.0%; Score 296.5; DB 7; Length 92;  
 Best Local Similarity 56.5%; Pred. No. 7.8e-28;  
 Matches 52; Conservative 19; Mismatches 20; Indels 1; Gaps 1;  
 QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNFVVDYETSSLSQ 60  
 Db 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPTACCFSTSRQIPQNFADYFETSSQCSK 59  
 QY 61 PAVVFTKRSKQVCAADPSEWQYVYDLELN 92  
 Db 60 PGVIFLTRKGRQVCAADPSEWQYVYDLELN 91

RESULT 13  
 US-10-332-038A-8  
 ; Sequence 8, Application US/10332038A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gryphon Therapeutics, Inc.  
 ; APPLICANT: Offord, Robin  
 ; APPLICANT: Gaertner, Hubert  
 ; APPLICANT: Hartley, Oliver  
 ; TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use  
 ; FILE REFERENCE: 03504.271  
 ; CURRENT APPLICATION NUMBER: US/10/332,038A  
 ; CURRENT FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: US 60/217,683  
 ; PRIOR FILING DATE: 2000-07-12  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 8  
 ; LENGTH: 70  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-332-038A-8

Query Match 57.2%; Score 278; DB 6; Length 70;  
 Best Local Similarity 58.1%; Pred. No. 8.6e-26;  
 Matches 47; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
 QY 24 APMGSDPPTACCFSTARKLPNFVVDYETSSLSQPAVFTKRSKQVCAADPSEWQ 83  
 Db 1 ASLAADTPTACCFSTSRQIPQNFADYFETSSQCSKPGVIFLTRKRSQVCAADPSEWQ 60  
 QY 84 EYVYDLELN 92

Db 61 KYVSDLELS 69  
: || ||| :

## RESULT 14

US-10-398-457-31  
; Sequence 31, Application US/10398457  
; GENERAL INFORMATION:  
; APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
; TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
; FILE REFERENCE: WO465  
; CURRENT APPLICATION NUMBER: US/10/398,457  
; CURRENT FILING DATE: 2003-11-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 31  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-398-457-31

Query Match 57.2%; Score 278; DB 6; Length 70;  
Best Local Similarity 68.1%; Pred. No. 8.6e-26;  
Matches 47; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 24 APMGSDPTACCFSTARKLPNFVVDYETSSLCQSPAVVFTKSKQVCADPSESVMQ 83  
Db 1 ASLAADTPTACCFSTYRSQIPQNFADYFETSSQCSKAPGVIFLTRSRQVCADPSESVMQ 60  
QY 84 EYVDLELN 92  
Db 61 KYVSDLELS 69  
: || ||| :

## RESULT 15

PCT-US03-28745-3  
; Sequence 3, Application PC/TUS0328745  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: PCT/US03/28745  
; CURRENT FILING DATE: 2003-09-11  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 3  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
PCT-US03-28745-3

Query Match 56.6%; Score 275; DB 1; Length 69;  
Best Local Similarity 68.7%; Pred. No. 1.9e-25;  
Matches 46; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 26 MGSDDPTACCFSTARKLPNFVVDYETSSLCQSPAVVFTKSKQVCADPSESVMQ 85  
Db 2 LAADTPTACCFSTYRSQIPQNFADYFETSSQCSKAPGVIFLTRSRQVCADPSESVMQ 61  
QY 86 VYDLELN 92  
Db 62 VSDLELS 68  
: || ||| :

Search completed: December 16, 2003, 15:47:23  
Job time : 14.5738 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 16, 2003, 15:39:40 ; Search time 24.6339 Seconds  
(without alignments)  
694.592 Million cell updates/sec

Title: US-09-920-137A-7

Perfect score: 486  
Sequence: 1 MKLCVTVLSLLMLVAAPFCSP.....VCADPSESWSVQYVVDLELN 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	486	100.0	92	11	US-09-834-794A-31
4	486	100.0	92	11	US-09-920-137A-7
5	486	100.0	92	12	US-10-137-655-7
6	486	100.0	92	14	US-10-158-366-4
7	486	100.0	92	14	US-10-057-275-7
8	486	100.0	92	15	US-10-293-705-11
9	461	94.9	92	11	US-09-771-023-11
10	394	81.1	92	14	US-10-114-482-3
11	375	77.2	69	10	US-09-792-793A-30
12	375	77.2	69	12	US-10-375-209A-30
13	371	76.3	68	9	US-09-195-457-10
14	320	65.8	93	9	US-08-927-939-49
15	320	65.8	93	9	US-09-151-450-2

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16 320 65.8 93 9 US-09-834-795A-32
17 320 65.8 93 11 US-09-834-794A-32
18 320 65.8 93 12 US-10-260-370-3
19 320 65.8 93 12 US-10-223-081-330
20 320 65.8 93 12 US-10-223-082-330
21 320 65.8 93 12 US-10-247-671-179
22 320 65.8 93 14 US-10-141-965-6
23 320 65.8 93 15 US-10-223-085-330
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25 320 65.8 93 15 US-10-223-088-330
26 320 65.8 93 15 US-10-223-090-330
27 320 65.8 93 15 US-10-223-087-330
28 320 65.8 93 15 US-10-223-083-330
29 320 65.8 93 15 US-10-223-089-330
30 315 64.8 93 12 US-10-301-822-179
31 300.5 61.8 92 8 US-08-927-939-19
32 300.5 61.8 92 9 US-09-151-450-3
33 300.5 61.8 92 9 US-09-908-599-3
34 300.5 61.8 92 9 US-09-334-923A-53
35 300.5 61.8 92 9 US-09-834-795A-33
36 300.5 61.8 92 9 US-09-334-954A-53
37 300.5 61.8 92 9 US-09-908-600-3
38 300.5 61.8 92 11 US-09-834-794A-33
39 300.5 61.8 92 11 US-09-920-137A-6
40 300.5 61.8 92 12 US-10-137-655-6
41 300.5 61.8 92 12 US-10-285-572-3
42 300.5 61.8 92 12 US-10-165-233A-53
43 300.5 61.8 92 12 US-10-116-275-221
44 300.5 61.8 92 14 US-10-158-366-3
45 300.5 61.8 92 14 US-10-057-275-6
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#### ALIGNMENTS

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RESULT 1
US-08-927-939-20
; Sequence 20, Application US/08927939
; Publication No. US20010008640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauren Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-20
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Query Match 100.0%; Score 486; DB 8; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKLCVTVLSLLMLVAAPFCSPALSGPDSPTACCFSTYARKLPNFWVDYETSSLCSQ 60
Db 1 MKLCVTVLSLLMLVAAPFCSPALSGPDSPTACCFSTYARKLPNFWVDYETSSLCSQ 60
Qy 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92
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RESULT 2
US-09-834-795A-31
; Sequence 31, Application US/09834795A
; Patent No. US20020076710A1
; GENERAL INFORMATION:
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; APPLICANT: Lawrence, Papsidero
; APPLICANT: Lyn, Dyster
; APPLICANT: Jana, Frustaci
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; FILE REFERENCE: 3380/11127-US3
; CURRENT APPLICATION NUMBER: US/09/834,795A
; PRIORITY FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 09/146,580
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/071,899
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 60/092,155
; PRIOR FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-795A-31

Query Match      100.0%; Score 486; DB 9; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNPNFVVDYETSSLSQ 60
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNPNFVVDYETSSLSQ 60
QY 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92

RESULT 3
US-09-834-794A-31
; Sequence 31, Application US/09834794A
; Publication No. US20030026777A1
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Papsidero
; APPLICANT: Lyn, Dyster
; APPLICANT: Jana, Frustaci
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; CURRENT APPLICATION NUMBER: US/09/834,794A
; PRIORITY FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/146,580
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/071,899
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 60/092,155
; PRIOR FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-794A-31

Query Match      100.0%; Score 486; DB 11; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNPNFVVDYETSSLSQ 60
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNPNFVVDYETSSLSQ 60
QY 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92

US-09-920-137A-7
; Sequence 7, Application US/09920137A
; Publication No. US20030049725A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Bandman, Olga
; APPLICANT: Wilde, Craig G.
; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/920,137A
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0027 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: MIP-1b
; US-09-920-137A-7

Query Match      100.0%; Score 486; DB 11; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNPNFVVDYETSSLSQ 60
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNPNFVVDYETSSLSQ 60
QY 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92

RESULT 5
US-10-137-655-7
; Sequence 7, Application US/10137655
; Publication No. US20030138917A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Bandman, Olga
; APPLICANT: Wilde, Craig G.
; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.

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LIBRARY: GenBank  
 CLONE: MIP-1b  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-10-057-275-7

Query Match 100.0%; Score 486; DB 14; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-48;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAFCSALSPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSQ 60  
 DB 1 MKLCVTLSLLMLVAAFCSALSPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSQ 60  
 QY 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92  
 DB 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92

## RESULT 8

US-10-293-705-11  
 ; Sequence 11, Application US/10293705  
 ; Publication No. US20030083468A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wilde, Craig G.  
 ; APPLICANT: Hawkins, Phillip R.  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Selthamer, Jeffrey J.  
 ; TITLE OF INVENTION: DNA ENCODING LIVER EXPRESSED CHEMOKINE  
 ; FILE REFERENCE: PF-0024-3 CON  
 ; CURRENT APPLICATION NUMBER: US/10/293,705  
 ; PRIOR FILING DATE: 2002-11-12  
 ; PRIOR APPLICATION NUMBER: 09/208,803  
 ; PRIOR FILING DATE: 1998-12-09  
 ; PRIOR APPLICATION NUMBER: 08/798,143  
 ; PRIOR FILING DATE: 1997-02-10  
 ; PRIOR APPLICATION NUMBER: 08/347,492  
 ; PRIOR FILING DATE: 1994-11-29  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 11  
 ; LENGTH: 92  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: GenBank ID No. US20030083468A1 g127080  
 US-10-293-705-11

Query Match 100.0%; Score 486; DB 15; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-48;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAFCSALSPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSQ 60  
 DB 1 MKLCVTLSLLMLVAAFCSALSPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSQ 60  
 QY 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92  
 DB 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92

## RESULT 9

US-09-771-023-11  
 ; Sequence 11, Application US/09771023  
 ; Publication No. US20030027990A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hardiman, Gerard T.  
 ; APPLICANT: Rossi, Devora L.  
 ; APPLICANT: Bacon, Kevin B.  
 ; APPLICANT: Bazar, J. Fernando  
 ; APPLICANT: Schall, Thomas J.  
 ; APPLICANT: Zlotnik, Albert  
 ; TITLE OF INVENTION: MAMMALIAN CX3C CHEMOKINE GENES

NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/771,023  
 FILING DATE: 2001-01-25  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/786,068  
 FILING DATE: 1997-01-21  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/590,828  
 FILING DATE: 24-JAN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0569K2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 92 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-771-023-11

Query Match 94.9%; Score 461; DB 11; Length 92;  
 Best Local Similarity 92.4%; Pred. No. 4.4e-45;  
 Matches 85; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAFCSALSPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSQ 60  
 DB 1 MKLCVSALSLLMLVAAFCSALSPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSQ 60  
 QY 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92  
 DB 61 PAVVFQTKRSKQVCADPSESWMQYVVDLELN 92

## RESULT 10

US-10-114-482-3  
 ; Sequence 3, Application US/10114482  
 ; Publication No. US20020150992A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wei et al.  
 ; TITLE OF INVENTION: Chemokine Alpha-5  
 ; FILE REFERENCE: PF401D1  
 ; CURRENT APPLICATION NUMBER: US/10/114,482  
 ; CURRENT FILING DATE: 2002-04-03  
 ; PRIOR APPLICATION NUMBER: 09/195,106  
 ; PRIOR FILING DATE: 1998-11-18  
 ; PRIOR APPLICATION NUMBER: 60/066,369  
 ; PRIOR FILING DATE: 1997-11-21  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 92  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-114-482-3

Query Match 81.1%; Score 394; DB 14; Length 92;  
 Best Local Similarity 77.2%; Pred. No. 1.9e-37;  
 Matches 71; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAARCSFALSNPMGSDPPTACCFSTARKLPNPFVVDYETSSLSQ 60  
 Db 1 MKLCVSFSLLLVAARCDVSLGAPICSDPPTSCCFSTARKIHRNFVMDYETSSLSQ 60

QY 61 PAVVFTKRSKQVADPSESQVQVYVDLELN 92  
 Db 61 PAVVFLTKGRQICADPEPWNVEYVDLELN 92

RESULT 11  
 US-09-792-793A-30  
 ; Sequence 30, Application US/09792793A  
 ; Patent No. US20020168370A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McDonald, John R.  
 ; APPLICANT: Coggin, Philip  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
 ; FILE REFERENCE: 25020-601D  
 ; CURRENT APPLICATION NUMBER: US/09/792,793A  
 ; CURRENT FILING DATE: 2001-02-22  
 ; NUMBER OF SEQ ID NOS: 93  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 30  
 ; LENGTH: 69  
 ; TYPE: PRT  
 ; ORGANISM: homo sapien  
 ; FEATURE:  
 ; OTHER INFORMATION: Human Chemokine Polypeptide: MIP-1-Beta  
 US-09-792-793A-30

Query Match 77.2%; Score 375; DB 10; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 APWGSDPPTACCFSTARKLPNPFVVDYETSSLSQPAVVFQTKRSKQVADPSESQVQ 83  
 Db 1 APWGSDPPTACCFSTARKLPNPFVVDYETSSLSQPAVVFQTKRSKQVADPSESQVQ 60

QY 84 EYVDLELN 92  
 Db 61 EYVDLELN 69

RESULT 12  
 US-10-375-209A-30  
 ; Sequence 30, Application US/10375209A  
 ; Publication No. US20030215421A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McDonald, John R.  
 ; APPLICANT: Coggin, Philip  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
 ; FILE REFERENCE: 25020-601E  
 ; CURRENT APPLICATION NUMBER: US/10/375,209A  
 ; CURRENT FILING DATE: 2003-02-24  
 ; NUMBER OF SEQ ID NOS: 93  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 30  
 ; LENGTH: 69  
 ; TYPE: PRT  
 ; ORGANISM: homo sapien  
 ; FEATURE:  
 ; OTHER INFORMATION: Human Chemokine Polypeptide: MIP-1-Beta  
 US-10-375-209A-30

Query Match 77.2%; Score 375; DB 12; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 APWGSDPPTACCFSTARKLPNPFVVDYETSSLSQPAVVFQTKRSKQVADPSESQVQ 83  
 Db 1 APWGSDPPTACCFSTARKLPNPFVVDYETSSLSQPAVVFQTKRSKQVADPSESQVQ 60

QY 84 EYVDLELN 92  
 Db 61 EYVDLELN 69

RESULT 13  
 US-09-195-457-10  
 ; Sequence 10, Application US/09195457  
 ; Patent No. US20020081623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILLIAMS, TIMOTHY J.  
 ; APPLICANT: JOSE, PETER J.  
 ; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.  
 ; APPLICANT: HSUAN, JOHN J.  
 ; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE  
 ; FILE REFERENCE: 550-33  
 ; CURRENT APPLICATION NUMBER: US/09/195,457  
 ; CURRENT FILING DATE: 1998-11-18  
 ; PRIOR APPLICATION NUMBER: 08/470,323  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR APPLICATION NUMBER: PCT/GB94/02006  
 ; PRIOR FILING DATE: 1994-09-14  
 ; PRIOR APPLICATION NUMBER: GB 9318984.3  
 ; PRIOR FILING DATE: 1993-09-14  
 ; PRIOR APPLICATION NUMBER: GB 94086902.2  
 ; PRIOR FILING DATE: 1994-04-29  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SEQ ID NO 10  
 ; LENGTH: 68  
 ; TYPE: PRT  
 ; ORGANISM: human  
 US-09-195-457-10

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 Best Local Similarity 100.0%; Pred. No. 5.8e-35;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PMGSDPPTACCFSTARKLPNPFVVDYETSSLSQPAVVFQTKRSKQVADPSESQVQ 84  
 Db 1 PMGSDPPTACCFSTARKLPNPFVVDYETSSLSQPAVVFQTKRSKQVADPSESQVQ 60

QY 85 YVDLELN 92  
 Db 61 YVDLELN 68

RESULT 14  
 US-08-927-939-49  
 ; Sequence 49, Application US/08927939  
 ; Publication No. US20010006640A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Grainger, David J.  
 ; APPLICANT: Tatalick, Lauen Marie  
 ; TITLE OF INVENTION: Compounds and methods to inhibit or  
 ; FILE REFERENCE: 295.022US1  
 ; CURRENT APPLICATION NUMBER: US/08/927,939  
 ; CURRENT FILING DATE: 1997-09-11  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 49  
 ; LENGTH: 93  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-08-927-939-49

Query Match 65.8%; Score 320; DB 8; Length 93;



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OM protein - protein search, using sw model

Run on: December 16, 2003, 15:36:19 ; Search time 36.6995 Seconds  
(without alignments)  
397.904 Million cell updates/sec

Title: US-09-920-137A-7

Perfect score: 486  
Sequence: 1 MKLCVTLSLLMLVAAPFCSP.....VCADESESWQVYVDLELN 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	92	11 AAR04220	Act-2 clone gene p
2	486	100.0	92	11 AAR05900	Act-2 gene product
3	486	100.0	92	13 AAR22712	Human MIP-1 alpha
4	486	100.0	92	16 AAR70798	MIP-1-beta. Homo
5	486	100.0	92	19 AAW76225	Human chemokine MI
6	486	100.0	92	20 AA82217	Human Act-2 protei
7	486	100.0	92	21 AAB15789	Human chemokine MI
8	486	100.0	92	23 AAM52445	HIV Nef1 fusion pr
9	486	100.0	92	23 AAM52446	HIV_Nef1 fusion pr

10	486	100.0	331	19 AAW76223	Human chemokine MI
11	483	99.4	92	23 ABP65219	Hypoxia-regulated
12	482	98.2	92	23 AAM52447	HIV_Nef1 fusion pr
13	478	98.4	92	24 ABUS2388	Human GPCR related
14	476	97.9	92	14 AAR36770	MIP-1-beta. Homo s
15	468	96.3	92	23 ABP62996	Human polypeptide
16	465.5	95.8	93	11 AAR05903	pAT 744 gene produ
17	463	95.3	92	24 ABUS2387	Human GPCR related
18	457	94.0	92	23 AAM52448	HIV Nef1 fusion pr
19	455	93.6	92	11 AAR04222	pAT744 gene produc
20	443.5	91.3	87	22 AAU02912	Angiotensin conver
21	441.5	90.8	91	10 AAP91030	Human H400 polypep
22	394	81.1	92	20 AAY42166	Rat MIP1-beta prot
23	385	79.2	92	10 AAP93591	Deduced sequence o
24	379	78.0	70	20 AAY14226	Chemokine hMCp1b.
25	379	78.0	70	20 AAY14227	Chemokine RANTES.
26	379	78.0	73	24 ABUS2390	Human GPCR related
27	379	78.0	73	24 ABUS2391	Human GPCR related
28	375	77.2	69	21 AAY88332	Human macrophage i
29	375	77.2	69	21 AAY69040	Amino acid sequenc
30	375	77.2	69	23 AAO21106	MIP-1 beta chemoki
31	375	77.2	69	23 AAO20014	Human chemokine MI
32	375	77.2	69	23 AAO14147	Human MIP-1beta pr
33	375	77.2	73	24 ABUS2389	Human GPCR related
34	375	77.2	74	14 AAR38925	ACT-2. Synthetic
35	375	77.2	92	18 AAW01805	Murine macrophage-
36	357	73.5	69	23 AAO21083	Protein of triple
37	320.5	65.9	92	23 AAE22580	Mouse lymphokine m
38	320	65.8	93	12 AAR11553	Human Stem Cell In
39	320	65.8	93	12 AAR14915	LD78beta. Homo sa
40	320	65.8	93	15 AAR62616	Stem cell inhibito
41	320	65.8	93	15 AAR62617	Variant stem cell
42	320	65.8	93	16 AAR70797	MIP-1-alpha. Homo
43	320	65.8	93	20 AAW82721	Human M110 protein
44	320	65.8	93	21 AAB15807	Human chemokine C1
45	320	65.8	93	21 AAY96281	Human chemokine MI

ALIGNMENTS

RESULT 1

AAR04220

ID AAR04220 standard; protein; 92 AA.

XX AAR04220;

XX AC

XX DT 25-MAR-2003 (updated)

XX DT 17-DEC-2001 (updated)

XX DT 12-SEP-1990 (first entry)

XX DE Act-2 clone gene product is activated human peripheral blood

XX DE mononuclear cell (PBMC).

XX KW Peripheral blood mononuclear cell; PBMC; lymphokine;

XX KW cytokine; mitogen; ds.

XX OS Homo sapiens.

XX PN USN7312001-N.

XX PD 13-MAR-1990.

XX PF 16-DEC-1988; 88US-0312001.

XX PR 16-DEC-1988; 88US-0312001.

XX PA (USHS ) US DBPT HEALTH & HUMAN SERVICE.

XX PA (USDC ) US SEC OF COMMERCE.

XX PI Siebenlist U, Leonard WJ, Zipfel PJ, Irving SG, Kelly K;

XX WPI; 1990-139708/18.

DR N-PSDB; AAQ03682.

XX New lymphokine-cytokine genes -

PT isolated using mRNA from activated human peripheral blood

PT mononuclear cells and T cells.

XX

PS Disclosure; Page?: 84pp; English.

XX

CC The lymphokine/cytokine-like proteins are associated with the

CC inflammatory response and/or have mitogenic activities. Antigens

CC raised to the proteins may be useful in detection and purification,

CC especially in bioassays of various tumour cells or genetic defects

CC in the inflammatory response.

CC (Note: Revised entry submitted to correct the patent number format of

CC US Government-owned NTIS applications to prevent clashes with ongoing US

CC granted patent numbers. For further information please visit the Derwent

CC web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 92 AA;

Query Match 100.0%; Score 486; DB 11; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.4e-49;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60

Db 1 MKLCVTVLSLLMLVAAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESVMQEVYVDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESVMQEVYVDLELN 92

RESULT 2

AA05900

ID AAR05900 standard; protein; 92 AA.

XX

AC AAR05900;

XX

DT 27-NOV-1990 (first entry)

XX

DE Act-2 gene product.

XX

KW Act-2; human lymphokine/cytokine-like protein; mitogenic; ds.

XX

OS Homo sapiens.

XX

PN WO9007009-A.

XX

PD 28-JUN-1990.

XX

PF 15-DEC-1989; 89WO-US05603.

XX

PR 16-DEC-1988; 88US-0285489.

XX

PA (USDC ) US SEC OF COMMERCE.

XX

PI SIEBENLIST U, ZIPPEL PE, KELLEY K, IRVING SG, NAPOLITANO M;

XX

PT LEONARD WJ;

XX

DR WPI; 1990-224535/29.

XX

DR N-PSDB; AAQ05297.

XX

PT New lymphokine-cytokine-like genes - isolated by subtraction

PT cloning and hybridisation using mRNA from activated peripheral

PT blood T cells.

XX

PS Disclosure; Page ?; 137pp; English.

XX

CC Probes raised to the gene product may be used in bioassay of the

CC product, useful in detecting tumour cells, genetic defects in the

CC inflammatory response, or in vivo, for the detection of immune

CC system activation. The proteins may also be used to determine the

CC presence of their receptors.

XX

SQ Sequence 92 AA;

Query Match 100.0%; Score 486; DB 11; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.4e-49;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60

Db 1 MKLCVTVLSLLMLVAAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYVYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESVMQEVYVDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESVMQEVYVDLELN 92

RESULT 3

AA02712

ID AAR22712 standard; Protein; 92 AA.

XX

AC AAR22712;

XX

DT 25-MAR-2003 (updated)

XX

DT 22-SEP-1992 (first entry)

XX

DE Human MIP-1 alpha.

XX

KW Macrophage inducible protein; cancer diagnosis; infection;

XX

KW myelopoietic dysfunction; autoimmune disease; ss.

XX

OS Homo sapiens.

XX

PN WO9205198-A.

XX

PD 02-APR-1992.

XX

PF 13-SEP-1991; 91WO-US06489.

XX

PR 14-SEP-1990; 90US-0582636.

XX

PA (CHIR ) CHIRON CORP.

XX

PI Tekampolso P, Gallegos CA;

XX

DR WPI; 1992-132088/16.

XX

DR N-PSDB; AAQ23729.

XX

PT Expression of pure mammalian macrophage inducible proteins in

PT yeast - to produce MIP for treatment and diagnosis of cancer,

PT infection, myelopoietic dysfunction, etc.

XX

PS Example 3; Fig 1; 38pp; English.

XX

CC This sequence was deduced from the nucleotide sequence AAQ23729.

CC The protein was produced by cloning into the expression vector

CC pVMP300. The human MIP-1alpha sequence was derived from the

CC lambda gt10 cDNA clone hMIP1-13a, and the GAPDH promoter sequence,

CC alpha factor transcription terminator derived from plasmid pGALL,

CC the construction of which is described in patent application

CC EP0324-274. Recombinantly produced MIP proteins have diagnostic and

CC therapeutic utility for detecting and treating infections, cancer,

CC myelopoietic dysfunction and autoimmune diseases. Although not

CC directly cytotoxic for WEHI tumor cells, MIP-1 treated macrophages

CC exhibited enhanced antibody-independent macrophage cytotoxicity for

CC tumour targets. MIP-1 treatment stimulated proliferation of mature

CC tissue macrophages; this effect was synergistic with both CSF-1 and

CC GM-CSF. Purified preparations of the recombinantly derived

CC MIP-1alpha peptide alone induced TNF and IL-6 in macrophages, but

CC MIP-1beta did not. As little as twofold excess MIP-1beta blocked

CC TNF-induction by MIP-1alpha to a significant degree. Other

CC bioactivity defined for native MIP-1 and recombinant MIP-1alpha



CC is the inhibition of proliferation of less differentiated  
 CC erythropoietin IL-3 dependent hematopoietic progenitor cells.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 92 AA;

Query Match 100.0%; Score 486; DB 13; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-49;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAPCSALSPAGSDPTACCFSTARKLPNFWVDYVYETSLCSQ 60  
 DB 1 MKLCVTLSLLMLVAAPCSALSPAGSDPTACCFSTARKLPNFWVDYVYETSLCSQ 60  
 QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
 DB 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 4  
 AAR70798  
 ID AAR70798 standard; Protein; 92 AA.  
 XX  
 AC AAR70798;

XX 25-MAR-2003 (updated)  
 DT 23-AUG-1995 (first entry)  
 XX MIP-1-beta.  
 XX Macrophage inflammatory protein 1-beta; MIP-1-beta;  
 KW heparanase; heparin; heparan sulfate; arthritis; restenosis;  
 KW cancer; wound healing.  
 XX Homo sapiens.

XX WO9504158-A1.  
 XX 09-FEB-1995.  
 XX 26-JUL-1994; 94WO-US08207.  
 XX 29-JUL-1993; 93US-0099866.  
 PR 13-OCT-1993; 93US-0136117.  
 XX (UPJO ) UPJOHN CO.  
 PA Hoogwerf AJ, Ledbetter SR;  
 PI WPI; 1995-082239/11.  
 DR N-PSDB; AAQ85368.

XX Screening for cpds. with anti-heparanase activity - by detecting  
 PT inhibition of heparin or heparan sulphate degradation,  
 PT potentially useful for treating arthritis, restenosis, cancer.  
 XX Claim 13; Page 47; 60pp; English.  
 XX Purified heparanases, prepared under reducing conditions and  
 CC activated with transglutaminase, are given in AAR70786-804. Most  
 CC are prepared by reverse transcription of mRNA from activated human  
 CC leukocytes, then cloning of the cDNA into pVL1392 baculovirus  
 CC vector, and expression in Sf9 cells in the presence of reduced  
 CC glutathione and dithiothreitol.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 92 AA;

Query Match 100.0%; Score 486; DB 16; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-49;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAPCSALSPAGSDPTACCFSTARKLPNFWVDYVYETSLCSQ 60  
 DB 1 MKLCVTLSLLMLVAAPCSALSPAGSDPTACCFSTARKLPNFWVDYVYETSLCSQ 60  
 QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
 DB 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

Query Match 100.0%; Score 486; DB 19; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-49;

QY 1 MKLCVTLSLLMLVAAPCSALSPAGSDPTACCFSTARKLPNFWVDYVYETSLCSQ 60  
 DB 1 MKLCVTLSLLMLVAAPCSALSPAGSDPTACCFSTARKLPNFWVDYVYETSLCSQ 60  
 QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
 DB 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 5  
 AAW76225  
 ID AAW76225 standard; Protein; 92 AA.  
 XX  
 AC AAW76225;  
 XX 02-DEC-1998 (first entry)  
 XX Human chemokine MIP-1beta domain protein fragment.

XX Chemokine; MIP-1beta; chimeric; human; heterologous protein; inhibitor;  
 KW receptor; chemotaxis; migratory cell; angiogenesis; bone; regeneration;  
 KW cartilage; ligament; tendon; bone marrow; transplant; inflammation;  
 KW autoimmune disorder; vaccine adjuvant; antigen presenting cell; cancer;  
 KW HIV; human immunodeficiency virus; therapy; prevention.

XX Homo sapiens.  
 OS Synthetic.  
 XX WO9838212-A2.  
 XX 03-SEP-1998.  
 XX 27-FEB-1998; 98WO-US04002.  
 PF 28-FEB-1997; 97US-0808720.  
 PR (GENY ) GENETICS INST INC.  
 PA Herrmann SH, Swanberg SL;  
 PI WPI; 1998-495387/42.

XX New chimeric polypeptide(s) - comprise chemokine polypeptide  
 PT covalently linked to heterologous polypeptide, used for, e.g.  
 PT chemotactic recruitment of migratory cells  
 XX Example 1; Page 53; 69pp; English.  
 XX This sequence represents a human chemokine MIP-1beta domain, derived  
 CC from HUMACT2A. This sequence is used in the production of a construct  
 CC comprising an isolated polynucleotide encoding a chimeric polypeptide  
 CC which comprises at least 1 chemokine polypeptide covalently attached to  
 CC at least 1 heterologous polypeptide. By including a heterologous protein  
 CC in the construction, the chimeric polypeptides will have longer and  
 CC increased biological activity and can direct the chemokine to a  
 CC particular site. The chimeric polypeptides can also be designed to  
 CC inhibit or desensitize chemokine receptors. They can be used to affect  
 CC the chemotactic recruitment of migratory cells, e.g. for stimulating or  
 CC inhibiting angiogenesis, for regeneration of bone, cartilage, ligament or  
 CC tendon, for recruiting transplanted bone marrow cells to bone marrow, or  
 CC for treating or preventing inflammatory or autoimmune disorders. They can  
 CC also be used as vaccine adjuvants or to enhance the activity of antigen  
 CC presenting cells and for treating or preventing HIV infection.  
 CC Neutralising antibodies binding to the chimeric polypeptide may also be  
 CC useful therapeutics for both conditions associated with the chemokine  
 CC corresponding to the chemokine domain of the chimeric polypeptide and  
 CC also in the treatment of some forms of cancer where abnormal expression  
 CC of the chemokine is involved.

XX Sequence 92 AA;

Query Match 100.0%; Score 486; DB 19; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-49;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNFWVDYVYETSSLSQ 60  
 DB 1 MKLCVTLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNFWVDYVYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCAFPSESQVQYVYDLELN 92  
 DB 61 PAVVFQTKRSKQVCAFPSESQVQYVYDLELN 92

RESULT 6  
 AAW82717  
 ID AAW82717 standard; Protein; 92 AA.  
 XX AC AAW82717;  
 XX DT 15-MAR-1999 (first entry)  
 XX DE Human Act-2 protein.  
 XX KW Chemokine; ZCHEMO-8; human; pathological condition; infection; cancer;  
 KW autoimmune disorder; immunodeficiency; myelopietic; wound healing;  
 KW transplant; progenitor cell; HIV infection; AIDS; chemotherapy;  
 KW radiation therapy; T cell; macrophage activation inhibitor; B lymphocyte;  
 KW chronic inflammatory disease; infective disease; diagnosis; detection;  
 KW drug screening; gene therapy; Act-2.  
 XX OS Homo sapiens.  
 XX KW WO9854326-A1.  
 XX PN 03-DEC-1998.  
 XX PD 19-MAY-1998; 98WO-US10329.  
 XX PF 29-MAY-1997; 97US-0047860.  
 XX PR (ZYMO) ZYMOGENETICS INC.  
 XX PA Sheppard PO;  
 XX PI WPI; 1999-059841/05.  
 XX DR New isolated human beta-chemokine, ZCHEMO-8 - used to develop  
 PT products for treating e.g. ischaemia, reperfusion, wound healing,  
 PT autoimmune diseases, inflammation, asthma or infections  
 XX Disclosure; Page 93; 131pp; English.

This sequence represents a human beta chemokine, Act-2 which is used to describe a method in which a novel beta chemokine, ZCHEMO-8 is isolated. Altered levels of ZCHEMO-8 may be indicative of pathological conditions, including infections, cancer, myelopietic disorders, autoimmune disorders and immunodeficiencies. The ZCHEMO-8 polypeptides can be used, e.g. to reduce the damage in ischaemic and reperfusion injuries, in a wound healing regime to stimulate an infiltration of immune cells (e.g. monocytes, neutrophils, T lymphocytes or basophils) to a wound site to facilitate healing. ZCHEMO may be used to mobilise progenitor cells from the marrow into the peripheral blood for transplants. ZCHEMO-8 polypeptides could be used to further define the role of chemokines in mediating suppression of HIV replication in CD4+ T-cells and limiting progression of HIV infection to AIDS. Use may be made of ZCHEMO-8 polypeptides during chemotherapy or radiation therapy, to protect haematopoietic cells. ZCHEMO-8 antagonists may have a beneficial therapeutic effect in diseases where the inhibition of activation of certain macrophages, neutrophils, basophils, B lymphocytes and/or T cells may be effective. Such diseases include autoimmune diseases e.g. multiple sclerosis, insulin-dependent diabetes and systemic lupus erythematosus. Rheumatoid arthritis, allergies, asthma or arteriosclerosis. Also benefit may be derived from using ZCHEMO-8 antagonists for chronic inflammatory and infective diseases. Antagonists may be used to dampen or inactivate ZCHEMO-8 during activated immune response. The products can also be used

CC for detection, diagnosis, drug screening or gene therapy.

XX Sequence 92 AA;

Query Match 100.0%; Score 486; DB 20; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.4e-49;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNFWVDYVYETSSLSQ 60  
 DB 1 MKLCVTLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNFWVDYVYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCAFPSESQVQYVYDLELN 92

DB 61 PAVVFQTKRSKQVCAFPSESQVQYVYDLELN 92

# RESULT 7

AA15789

ID AAB15789 standard; Protein; 92 AA.

XX AC AAB15789;

DT 17-JAN-2001 (first entry)

DE Human chemokine MIP1beta SEQ ID NO: 20.

XX KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;  
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;  
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;  
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;  
 KW rheumatoid arthritis; contraception.

XX OS Homo sapiens.

XX KW WO200042071-A2.

XX PD 20-JUL-2000.

XX PF 12-JAN-2000; 2000WO-US00821.

XX PR 12-JAN-1999; 99US-0229071.

XX PR 17-MAR-1999; 99US-0271192.

XX PR 01-DEC-1999; 99US-0452406.

XX PA (NEOR-) NEORX CORP.

XX PI Grainger DU, Tatalick LM;

XX DR WPI; 2000-499101/44.

XX DR N-PSDB; AAA74885.

XX PT New peptide 3, amide and heterocyclic compounds and saccharide  
 PT conjugates used for inhibiting chemokine induced activity and for  
 PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour  
 PT growth

XX Example 1; Page 134; 387pp; English.

XX The present invention concerns the identification of a number of  
 CC chemokines which can be used to produce derivatives, agonists and  
 CC antagonists which are then useful in disease treatment. The chemokines  
 CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.  
 CC These chemokine derivatives can be used to treat diseases such as  
 CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and  
 CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated  
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and  
 CC rheumatoid arthritis, and can be used to prevent strokes and as  
 CC contraceptive. The coding sequences for the chemokines can be used in  
 CC gene therapy for the same diseases, as well as in the production of  
 CC animal models.

XX Sequence 92 AA;



XX PH Key Location/Qualifiers  
 FT Peptide 1..24  
 FT /label= signal  
 FT /note= "signal peptide"  
 FT Protein 25..331  
 FT /label= MIP-lbata  
 FT /note= "Chemokine domain"  
 XX WO9838212-A2.  
 XX 03-SEP-1998.  
 XX 27-FEB-1998; 98WO-US04002.  
 XX 28-FEB-1997; 97US-0808720.  
 XX (GEMY ) GENETICS INST INC.  
 XX Herrmann SH, Swanberg SL;  
 XX PI  
 XX N-PSDB; AAV56825.  
 XX  
 PT New chimeric polypeptide(s) - comprise chemokine polypeptide  
 PT covalently linked to heterologous polypeptide, used for, e.g.  
 PT chemotactic recruitment of migratory cells  
 XX  
 PS Claim 16c; Page 50-51; 69pp; English.  
 XX  
 CC This sequence represents a human chemokine MIP-lbata domain, isolated  
 CC from cDNA clone WPB-X. This sequence is used in the production of a  
 CC construct comprising an isolated polynucleotide encoding a chimeric  
 CC polypeptide which comprises at least 1 chemokine polypeptide covalently  
 CC attached to at least 1 heterologous polypeptide. By including a  
 CC heterologous protein in the construction, the chimeric polypeptides will  
 CC have longer and increased biological activity and can direct the  
 CC chemokine to a particular site. The chimeric polypeptides can also be  
 CC designed to inhibit or desensitise chemokine receptors. They can be used  
 CC to affect the chemotactic recruitment of migratory cells, e.g. for  
 CC stimulating or inhibiting angiogenesis, for regeneration of bone,  
 CC cartilage, ligament or tendon, for recruiting transplanted bone marrow  
 CC cells to bone marrow, or for treating or preventing inflammatory or  
 CC autoimmune disorders. They can also be used as vaccine adjuvants or to  
 CC enhance the activity of antigen presenting cells and for treating or  
 CC preventing HIV infection. Neutralising antibodies binding to the chimeric  
 CC polypeptide may also be useful therapeutics for both conditions  
 CC associated with the chemokine corresponding to the chemokine domain of  
 CC the chimeric polypeptide and also in the treatment of some forms of  
 CC cancer where abnormal expression of the chemokine is involved.  
 XX  
 SQ Sequence 331 AA;  
 Query Match 100.0%; Score 486; DB 19; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-48;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLCVTVLSLLMLVAAFCSFALSPALSGDPTACCFSTARKLPNFVVDYVYETSSLCQ 60  
 DB 1 MKLCVTVLSLLMLVAAFCSFALSPALSGDPTACCFSTARKLPNFVVDYVYETSSLCQ 60  
 QY 61 PAVVFTKRSKQVCAADPSSESWQVYVYDLELN 92  
 DB 61 PAVVFTKRSKQVCAADPSSESWQVYVYDLELN 92  
 RESULT 11  
 ID ABP65219  
 XX ABP65219 standard; Protein; 92 AA.  
 AC ABP65219;  
 XX  
 DT 12-NOV-2002 (first entry)

XX Hypoxia-regulated protein #93.  
 DE  
 XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;  
 KW antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;  
 KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
 KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
 KW preclampsia; atherosclerosis; inflammatory condition; wound healing;  
 KW inflammation; erythropoiesis; hair loss; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200246465-A2.  
 XX 13-JUN-2002.  
 XX 10-DEC-2001; 2001WO-GB05458.  
 XX 08-DEC-2000; 2000GB-0030076.  
 XX 08-FEB-2001; 2001GB-0003156.  
 XX 25-OCT-2001; 2001GB-0025666.  
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;  
 PI Rayner MN;  
 XX  
 DR WPI; 2002-627238/67.  
 XX  
 PT Identifying a gene involved in disease for treating hypoxia-regulated  
 PT conditions, comprises comparing the transcriptome/protome of two cell  
 PT types under different conditions and identifying a differentially  
 PT regulated gene -  
 XX  
 PS Claim 35; Page 401; 538pp; English.  
 XX  
 CC The present invention relates to methods for identifying genes and  
 CC proteins that are implicated in a specific disease or physiological  
 CC condition. The method comprises comparing the transcriptome/protome of a  
 CC specialised cell type implicated in a disease or condition with that of a  
 CC second specialised cell type, under two experimental conditions, and  
 CC identifying a gene that is differentially regulated in the two  
 CC specialised cell types under experimental conditions. ABV77873-ABV78116  
 CC and ABP65061-ABP65257 were identified using the methods of the invention.  
 CC The coding sequences and proteins are useful for treating a disease in a  
 CC patient, for manufacture of a medicament for treating hypoxia-regulated  
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,  
 CC biological response to hypoxia conditions, or hypoxic-associated  
 CC pathology in a patient. The coding sequences and proteins are also useful  
 CC for monitoring the therapeutic treatment of a disease or physiological  
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,  
 CC retinopathy, neonatal stress, preclampsia, atherosclerosis, inflammatory  
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss.  
 XX  
 SQ Sequence 92 AA;  
 Query Match 99.4%; Score 483; DB 23; Length 92;  
 Best Local Similarity 98.9%; Pred. No. 9.9e-49;  
 Matches 91; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLCVTVLSLLMLVAAFCSFALSPALSGDPTACCFSTARKLPNFVVDYVYETSSLCQ 60  
 DB 1 MKLCVTVLSLLMLVAAFCSFALSPALSGDPTACCFSTARKLPNFVVDYVYETSSLCQ 60  
 QY 61 PAVVFTKRSKQVCAADPSSESWQVYVYDLELN 92  
 DB 61 PAVVFTKRSKQVCAADPSSESWQVYVYDLELN 92  
 RESULT 12  
 ID AAM52447  
 XX AAM52447 standard; Protein; 92 AA.  
 ID AAM52447  
 XX

AC AAM52447;  
 XX 03-JUL-2002 (first entry)  
 XX HIV\_Nef1 fusion protein #14.  
 XX Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.  
 XX Homo sapiens.  
 XX US6303295-B1.  
 XX 16-OCT-2001.  
 XX 12-JUL-1996; 96US-0679493.  
 XX 14-JUL-1995; 95US-001203P.  
 XX 01-SEP-1995; 95US-003112P.  
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
 XX Taylor EW, Nadimpalli RG, Ramanathan CS;  
 XX WPI; 2002-024734/03.  
 XX New selenoprotein for use in detecting certain viruses, e.g. human  
 XX immunodeficiency virus (HIV) or Ebola, cancer and immune system  
 XX disorders -  
 XX Disclosure; Columns 73-76; 140pp; English.  
 XX The present invention relates to selenoproteins encoded in the genome of  
 XX a virus, where the coding sequence of the selenoprotein is genetically  
 XX engineered for expression in a nucleic acid construct. The invention also  
 XX discloses a method for identifying selenoprotein coding sequences, for  
 XX detecting certain viruses (e.g. HIV or Ebola), cancer and immune system  
 XX disorders. The present sequence was used to illustrate the invention.  
 XX Sequence 92 AA;  
 XX  
 Query Match 99.2%; Score 482; DB 23; Length 92;  
 Best Local Similarity 98.9%; Pred. No. 1.3e-48;  
 Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLCVTVLSLLMLVAAFCSFSPALSPAGSDPPTACCFSTARKLPNFVVDYVETSLCSQ 60  
 Db 1 MKLCVTVLSLLMLVAAFCSFSPALSPAGSDPPTACCFSTARKLPNFVVDYVETSLCSQ 60  
 QY 61 PAVVFOTKSKOVCAQPSSESWQVYVDLELN 92  
 Db 61 PAVVFOTKSKOVCAQPSSESWQVYVDLELN 92  
 RESULT 13  
 ABUS2388  
 ID ABUS2388 standard; Protein; 92 AA.  
 XX  
 AC ABUS2388;  
 XX  
 XX 03-MAR-2003 (first entry)  
 XX Human GPCR related protein NOV36b.  
 XX Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytostatic.  
 XX Homo sapiens.  
 XX WO200279398-A2.  
 XX 10-OCT-2002.  
 XX 08-MAR-2002; 2002WO-US07355.  
 XX

PR 08-MAR-2001; 2001US-274194P.  
 PR 08-MAR-2001; 2001US-274281P.  
 PR 08-MAR-2001; 2001US-274322P.  
 PR 09-MAR-2001; 2001US-274849P.  
 PR 13-MAR-2001; 2001US-275578P.  
 PR 13-MAR-2001; 2001US-275579P.  
 PR 13-MAR-2001; 2001US-275601P.  
 PR 14-MAR-2001; 2001US-276000P.  
 PR 16-MAR-2001; 2001US-276776P.  
 PR 19-MAR-2001; 2001US-276994P.  
 PR 20-MAR-2001; 2001US-277239P.  
 PR 20-MAR-2001; 2001US-277327P.  
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 PR 09-NOV-2001; 2001US-332486P.  
 PR 09-NOV-2001; 2001US-345399P.  
 PR 07-MAR-2002; 2002US-0034886.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M, Burgess CE;  
 XX Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL, Guo X;  
 XX Shenoy SG, Padigaru M, Taupier RJ, Miller CE, Casman SJ, Pena CEA;  
 XX Gangolli EA, Gusev V, Smithson G, Zernusen BD, Gerlach V;  
 XX Pochart PF, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;  
 XX Larocheville WJ, Zhong M, Khramtsov NV, Voss EZ, Herrmann JL;  
 XX WPI; 2003-058423/05.  
 XX N-PSDB; ABX70479.  
 XX  
 XX NOVX polypeptides and polynucleotides, useful for treating a syndrome  
 XX related to a human disease associated with the NOVX polypeptide e.g.,  
 XX cancer -  
 XX  
 XX Claim 1; Page 202; 413pp; English.

The present invention relates to the isolation of novel human polypeptides referred to as NOVX (NOV1-NOV44), variants of these proteins, and the polynucleotide sequences encoding them. The NOVX proteins of the invention are G-protein coupled receptor (GPCR) related proteins. The sequences of the invention are useful in the manufacture of a medicament for treating a syndrome related to a human disease associated with the polypeptides e.g. cancer. ABUS2311-ABUS2408 represent the human NOVX proteins of the invention.

SQ Sequence 92 AA;

Query Match 98.4%; Score 478; DB 24; Length 92;  
 Best Local Similarity 97.8%; Pred. No. 3.8e-48;  
 Matches 90; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAPCSALSPALSGDPTACCFSTARKLPNPFVVDYETSSLSQ 60  
 DB 1 MKLCVTLSLLMLVAAPCSALSPALSGDPTACCFSTARKLPNPFVVDYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92  
 DB 61 PAVVFQTKRGKQVCADPSESWSVQEVYVDLELN 92

RESULT 14  
 ID AAR36770 standard; protein; 92 AA.  
 AC AAR36770;  
 XX 25-MAR-2003 (updated)  
 DT 29-SEP-1993 (first entry)  
 XX MIP-1beta.  
 XX Macrophage inflammatory protein; megakaryocytopoiesis; MIP-1; MIP-2;  
 KW thrombocythemia; reactive thrombocytosis; stroke; emboli; platelet;  
 KW myeloproliferative disorder.  
 XX Homo sapiens.  
 OS WO3309799-AL.  
 PN 27-MAY-1993.  
 PD 13-NOV-1992; 92WO-US09671.  
 FF 15-NOV-1991; 91US-0792988.  
 PR (UTYPE-) UNIV PENNSYLVANIA.  
 PA Gewirtz AM;  
 FI WPI; 1993-182239/22.  
 DR Suppression of megakaryocytopoiesis - by administration of  
 PT macrophage inflammatory protein-1 or -2  
 PS Disclosure; Page 17; 26pp; English.  
 XX A claimed method for reducing the no. of circulating platelets in the  
 CC bloodstream of a mammal comprises admin. of MIP-1 and/or MIP-2 or  
 CC their analogues to induce such a reduction. The MIP-1, MIP-2 or  
 CC analogue may be operatively linked to a carrier. The MIPs can be  
 CC used to inhibit megakaryocytopoiesis to effect in vivo reduction of  
 CC platelet nos. They can be used to treat disorders with excessively  
 CC high platelet counts such as thrombocytosis, stroke, pulmonary emboli  
 CC and myeloproliferative disorders.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 92 AA;

Query Match 97.9%; Score 476; DB 14; Length 92;  
 Best Local Similarity 98.9%; Pred. No. 6.5e-48;  
 Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAPCSALSPALSGDPTACCFSTARKLPNPFVVDYETSSLSQ 60  
 DB 1 MKLCVTLSLLMLVAAPCSALSPALSGDPTACCFSTARKLPNPFVVDYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92  
 DB 61 PAVVFQTKRGKQVCADPSESWSVQEVYVDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92

RESULT 15  
 ID ABP62996 standard; protein; 92 AA.  
 AC ABP62996;  
 XX 14-OCT-2002 (first entry)  
 DT Human polypeptide SEQ ID NO 433.  
 XX Human; vulnary; dermatological; neuroprotective; nootropic; cancer;  
 KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;  
 KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;  
 KW burn; central nervous system disorder; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; immune disorder;  
 KW autoimmune disorder; multiple sclerosis; diabetes; allergy.  
 XX Homo sapiens.  
 OS WO200218424-A2.  
 PN 07-MAR-2002.  
 PD 31-AUG-2001; 2001WO-US27093.  
 PF 01-SEP-2000; 2000US-0654935.  
 PR (HYSE-) HYSEQ INC.  
 PA Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
 FI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;  
 XX WPI; 2002-583321/62.  
 DR N-PSDB; ABQ93475.  
 XX New polynucleotide and polypeptides, useful for treatment and diagnosis  
 PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral  
 PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple  
 PT sclerosis, diabetes and allergies -  
 XX Claim 20; SEQ ID NO 433; 284pp + Sequence Listing; English.  
 CC The invention relates to an isolated polynucleotide (I) comprising one of  
 CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising  
 CC administering to a mammalian subject a composition comprising the protein  
 CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).  
 CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.  
 CC (I) is useful for gene therapy of diseases and (II) can be used for  
 CC therapeutic treatment. Diseases that may be treated include wound healing  
 CC and tissue repair, burns, central nervous system disorders (e.g.  
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral  
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple  
 CC sclerosis, diabetes and allergies.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 92 AA;

Query Match 96.3%; Score 468; DB 23; Length 92;  
 Best Local Similarity 96.7%; Pred. No. 5.6e-47;  
 Matches 89; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLCVTLSLLMLVAAPCSALSPALSGDPTACCFSTARKLPNPFVVDYETSSLSQ 60  
 DB 1 MKLCVTLSLLMLVAAPCSALSPALSGDPTACCFSTARKLPNPFVVDYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92  
 DB 61 PAVVFQTKRGKQVCADPSESWSVQEVYVDLELN 92

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